

/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by life technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 240 a 210 c 208 g 191 t 20 others

Query Match 43.7%; Score 798; DB 9; Length 869;
Best Local Similarity 96.3%; Pred. No. 7,1e-128;
Matches 836; Conservative 20; Mismatches 5; Indels 7; Gaps 4;

QY 2 GGGGATGTCCTGCTGCTGATTAAGCCCTGGCCGCTGTGACAGAGCCCGTACCCGAGA 61
DB 1 GGGGAGTCCCTGCTGCTGCTAAGCCCTGGCCGCTGTGACAGAGCCCGTACCCGAGA 60
QY 62 GCGGACCGTTCAATGTCGCTGTAAGCTGGAATCCAGAGTGAATGCTACAAACATGA 121
DB 61 GCGGACCGTTCAATGTCGCTGTAAGCTGGAATCCAGAGTGAATGCTACAAACATGA 120
QY 122 TCTAATCCCGGAGACTTGAAGGACCTCCGAGTGAACCTGTTACAACTAGTGTGCAAC 181
DB 121 TCTAATCCCGGAGACTTGAAGGACCTCCGAGTGAACCTGTTACAACTAGTGTGCAAC 180
QY 182 AGGGGACTATTCAATTTTGAATGAATGTAAGCTGGGTACTCCGGGAGATGCCAGATCCG 241
DB 181 AGGGGACTATTCAATTTTGAATGAATGTAAGCTGGGTACTCCGGGAGATGCCAGATCCG 240
QY 242 CTGTGTAAGGACCAAGATTTGTGAGGCGGCAAAAGCACTTCCAGTCTTACAGCTG 301
DB 241 CTGTGTAAGGACCAAGATTTGTGAGGCGGCAAAAGCACTTCCAGTCTTACAGCTG 300
QY 302 TGTGAGGT-GCAATTACACAGAGGCC---TTCAGATC-AGAACAAGCCCTGTGTG 355
DB 301 TGTGAGGTGCAATTACACAGAGGACATATCCAGTCTTACAGCCAGTCTGTG 360
QY 356 TAAATGACATTTTCTATATTCGGCTTCCCTGTGAGCTGAACAAGCTAT-TTCAATTG 414
DB 361 TAAATGACATTTTCTATATTCGGCTTCCCTGTGAGCTGAACAAGCTAT-TTCAATTG 420
QY 415 GGGCCCAATATTTCTTCAATGAATATGAATGAGTGGCCCTTCCAGTCTGTGAATT 474
DB 421 GGGCCCAATATTTCTTCAATGAATATGAATGAGTGGCCCTTCCAGTCTGTGAATT 480
QY 475 TCACCTCACCAGGCTGCTGACACATATGAATATTAATAAAGTGTGCAAGCCG 534
DB 481 TCACCTCACCAGGCTGCTGACACATATGAATATTAATAAAGTGTGCAAGCCG 540
QY 535 GAAGCTGTGGGATCCGAATCATCTGCTGTGAAGAAATGAGAGACATGTAAGTGA 594
DB 541 GAAGCTGTGGGATCCGAATCATCTGCTGTGAAGAAATGAGAGACATGTAAGTGA 600
QY 595 ACTTCAACCACTCCCTGCGGAAACAGATACATGGCTCTTATCCAAACAGAGACTATCA 654
DB 601 ACTTCAACCACTCCCTGCGGAAACAGATACATGGCTCTTATCCAAACAGAGACTATCA 660
QY 655 TCGGGTTTTCTCAGTGTGTTGAGCCACACAGAAAGAAACGCGAGCTTCAAGTGTGA 714
DB 661 TCGGGTTTTCTCAGTGTGTTGAGCCACACAGAAAGAAACGCGAGCTTCAAGTGTGA 720
QY 715 TTCAAGTACTGGGAGATGTAAGTGTGTAAGTGTGAGTCACTGACTCCATATTTTCTACT 774
DB 721 TTCAAGTACTGGGAGATGTAAGTGTGTAAGTGTGAGTCACTGACTCCATATTTTCTACT 780
QY 775 GGGGACGCACTGATCCGATTAAGGAAAGATGTCCTGCGCCCAACAAGGGCTCC 834
DB 781 GGGGACGCACTGATCCGATTAAGGAAAGATGTCCTGCGCCCAACAAGGGCTCC 840

QY 835 CTTTCCCTCTGATTAACAACAAGAACAA 862
DB 841 CTTTCCCTCTGATTAACAACAAGAACAA 868

RESULT 2
BI823321 946 bp mRNA linear EST 04-OCT-2001
LOCUS 603041231F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182255 5',
DEFINITION mRNA sequence.
ACCESSION BI823321
VERSION BI823321.1 GI:15934871
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 946)
NIH-MGC http://mgs.mci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov
Plate: LLM11454 row: m column: 08
High quality sequence stop: 795.
Location/Qualifiers
1. 946
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5182255"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH-MGC Library."

FEATURES
source 1. 946

BASE COUNT 240 a 239 c 243 g 224 t

Query Match 41.9%; Score 766.2; DB 13; Length 946;
Best Local Similarity 91.3%; Pred. No. 2,1e-122;
Matches 910; Conservative 0; Mismatches 33; Indels 54; Gaps 7;

QY 2 GGGGATGTCCTGCTGCTGATTAAGCCCTGGCCGCTGTGACAGAGCCCGTACCCGAGA 61
DB 1 GGGGATGTCCTGCTGCTGCTAAGCCCTGGCCGCTGTGACAGAGCCCGTACCCGAGA 60
QY 62 GCGGACCGTTCAATGTCGCTGTAAGCTGGAATCCAGAGTGAATGCTACAAACATGA 121
DB 61 GCGGACCGTTCAATGTCGCTGTAAGCTGGAATCCAGAGTGAATGCTACAAACATGA 120
QY 122 TCTAATCCCGGAGACTTGAAGGACCTCCGAGTGAACCTGTTACAACTAGTGTGCAAC 181
DB 121 TCTAATCCCGGAGACTTGAAGGACCTCCGAGTGAACCTGTTACAACTAGTGTGCAAC 180
QY 182 AGGGGACTATTCAATTTTGAATGAATGTAAGCTGGGTACTCCGGGAGATGCCAGATCCG 241
DB 181 AGGGGACTATTCAATTTTGAATGAATGTAAGCTGGGTACTCCGGGAGATGCCAGATCCG 240
QY 242 CTGTGTAAGGACCAAGATTTGTGTAAGGCGGCAAAAGCACTTCCAGTCTTACAGCTG 301


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QY 1549 CCTATCCCAACATTACAGGAAAGAAACGTTGATGATCCTGAAGCTTACTATGACGCT 1608
Db 177 CCTATCCCMCCAAATTACAGGMAAAACGTTGATGATCCTGAAGCTTACTATGACGCT 118
QY 1609 ACAAACAGCCTTAGTAATTAATAACATTTTATACCAATAAATTTTCAATATTAATACT 1668
Db 117 ACAAACAGCCTTAGTAATTAATAACATTTTATAMHWTAAATTTTCAATATTAATACT 58
QY 1669 AATGTAGCATTAACTAACGATTGGAACATACATTTCACACTTCAAAAGCTGTTTTATA 1725
Db 57 AATGTAGCATTAACTAACGATTGGAACCTCAATTCACACCCYCAAAGCTGTTTTATA 1

RESULT 4
LOCUS AV709899 703 bp mRNA linear EST 09-OCT-2000
DEFINITION AV709899 ADC Homo sapiens cDNA clone ADCAB04 5', mRNA sequence.
ACCESSION AV709899
VERSION AV709899.1 GI:10728055
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 703)
AUTHORS Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao
H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z.,
Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu
G., Hu, R., Chen, J., Chen, Z., and Han, Z.
Homo sapiens cDNA ADC clones
This clone is available at CHGC in Shanghai.
LOCATION/Qualifiers
1..703
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADCAB04"
/clone_lib="ADC"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
/Note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 186 a 172 c 166 g 177 t 2 others
ORIGIN
Query Match 35.3%; Score 645.4; DB 10; Length 703;
Best Local Similarity 97.5%; Pred. No. 1.4e-101;
Matches 655; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 280 GCAACTTCAGTCTCAGCTCAGCTGTGAGTGCAATTACACAGAGGCTTCCAGACTCAGA 339
Db 1 GCAACTTCAGTCTCAGCTCAGCTGTGAGTGCAATTACACAGAGGCTTCCAGACTCAGA 60
QY 340 CCAGACCCCTCTGGTGGTAATGGACATTTTCTATATCGGCTTCCTGTAGAGCTGAACA 399
Db 61 CCAGACCCCTCTGGTGGTAATGGACATTTTCTATATCGGCTTCCTGTAGAGCTGAACA 120
QY 400 CAGTCTATTTCATTTGGGGCCCAATAATTTCCTAATGCAAAATGAAATGAGATGCCCTT 459
Db 121 CAGTCTATTTCATTTGGGGCCCAATAATTTCCTAATGCAAAATGAAATGAGATGCCCTT 180
QY 460 CCATGCTCTGGAATTTTCACCTCACCAGGCTGCTAGACCACATAATGAATATAAAAAA 519
Db 181 CCATGCTCTGGAATTTTCACCTCACCAGGCTGCTAGACCACATAATGAATATAAAAAA 240

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RESULT 5

BM693867

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

BM693867 652 bp mRNA linear EST 28-FEB-2002
 UI-E-DW1-ah-e-i-22-0-UI.r1 UI-E-DW1 Homo sapiens cDNA clone
 UI-E-DW1-ah-e-i-22-0-UI 5', mRNA sequence.

BM693867
 BM693867.1 GI:19007125

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 652)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 Reverse.

Location/Qualifiers

1..652

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="UI-E-DW1-ah-e-i-22-0-UI"

/clone_lib="UI-E-DW1"

/tissue_type="lens"

/dev_stage="adult"

FEATURES

source

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: Ecor I; Site 2: Not I;
 UI-E-DWI is a normalized cDNA library containing the
 following tissue(s): lens. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an Ecor I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CGATTAGCGA. This library
 was created for the program, Gene Discovery in the Visual
 System, supported by National Eye Institute (NEI)."
 BASE COUNT 188 a 167 c 135 g 162 t
 ORIGIN

Query Match 34.9%; Score 638.4; DB 14; Length 652;
 Best Local Similarity 99.7%; Pred. No. 2.3e-100;
 Matches 650; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 Qy 961 AGAAGACTTCCCTTTTACACACACTACTGCCCCCATTAAGGTTCTGTGGTTTACC 1020
 Db 1 AGAAGACTTCCCTTTTACACACACTACTGCCCCCATTAAGGTTCTGTGGTTTACC 60
 Qy 1021 CATCTGAATATGTTTCCATCATCACAAATTTGTTACTTCTACTGAATTTCTCAAAACCAT 1080
 Db 61 CATCTGAATATGTTTCCATCATCACAAATTTGTTACTTCTACTGAATTTCTCAAAACCAT 120
 Qy 1081 GCAGAAGTCAGGTCACTCTTGAAGAGTGGCAGAAAAGAAAATAGCAGAGATGGGTCAG 1140
 Db 121 GCAGAAGTCAGGTCACTCTTGAAGAGTGGCAGAAAAGAAAATAGCAGAGATGGGTCAG 180
 Qy 1141 TGCAGTGGCTTGCCTCAAAAGAGCGCAGACAAAGTCGTCTCTCTTTTCCAAATG 1200
 Db 181 TGCAGTGGCTTGCCTCAAAAGAGCGCAGACAAAGTCGTCTCTCTTTTCCAAATG 240
 Qy 1201 AGCTCAACAGTGTGCGATGGTACCTGTGGCAAGCAGGCGCAGTCCAGTGAGAACT 1260
 Db 241 AGCTCAACAGTGTGCGATGGTACCTGTGGCAAGCAGGCGCAGTCCAGTGAGAACT 300
 Qy 1261 CTCAGACCTTTCCTCCCTTGCCTTTAACTTTTTCGAGTATCTAAGAACGACGATTC 1320
 Db 301 CTCAGACCTTTCCTCCCTTGCCTTTAACTTTTTCGAGTATCTAAGAACGACGATTC 360
 Qy 1321 ATCTGCACAAATACGTTGGTCTACTTTAGACAGATTGATACAAAGACGATTACAATG 1380
 Db 361 ATCTGCACAAATACGTTGGTCTACTTTAGACAGATTGATACAAAGACGATTACAATG 420
 Qy 1381 CTCTCAGTGTGCCCCCAAGTACCACTTCATGAAGGATGCCACTGTTCTGTGCAGAAC 1440
 Db 421 CTCTCAGTGTGCCCCCAAGTACCACTTCATGAAGGATGCCACTGTTCTGTGCAGAAC 480
 Qy 1441 TTCTCCATGTCAAGCAGCGGTGTACGAGGAAAAGATACAAAGCCTGCGACGATGGCT 1500
 Db 481 TTCTCCATGTCAAGCAGCGGTGTACGAGGAAAAGATACAAAGCCTGCGACGATGGCT 540
 Qy 1501 GCTGTCTCTTGTAGCCACCCATGAGAGCAGACGACCTTAAGGTTCTCTATCCACCA 1560
 Db 541 GCTGTCTCTTGTAGCCACCCATGAGAGCAGACGACCTTAAGGTTCTCTATCCACCA 600
 Qy 1561 ATTACAGGG-AAAAACGTTGATGATCTCTGAAGCTTACTATCGACCTTACA 1611
 Db 601 ATTACAGGGAAAAAACGTTGATGATCTCTGAAGCTTACTATCGACCTTACA 652

RESULT 6
 BM670929/c
 LOCUS
 DEFINITION UI-E-DWI-ah-e-i-22-0-UI.s1 UI-E-DWI Homo sapiens cDNA clone
 657 bp mRNA linear EST 27-FEB-2002
 UI-E-DWI-ah-e-i-22-0-UI 3', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 COMMENT

FEATURES
 source

BM670929
 BM670929.1 GI:18980826
 EST.
 Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (Bases 1 to 657)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 9704477
 Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9585
 Email: msoares@blue.weeg.uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 Forward
 POLVA=Yes.

Location/Qualifiers
 1..657
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 /clone="UI-E-DWI-ah-e-i-22-0-UI"
 /clone_lib="UI-E-DWI"
 /tissue_type="lens"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: Ecor I; Site 2: Not I;
 UI-E-DWI is a normalized cDNA library containing the
 following tissue(s): lens. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an Ecor I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CGATTAGCGA. This library
 was created for the program, Gene Discovery in the Visual
 System, supported by National Eye Institute (NEI).
 TAG LIB=UI-E-DWI
 TAG_TISSUE=human lens
 TAG_SEQ=CGATTAGCGA"

BASE COUNT 167 a 116 c 150 g 224 t
 ORIGIN

Query Match 34.5%; Score 630.6; DB 13; Length 657;
 Best Local Similarity 98.5%; Pred. No. 5e-99;
 Matches 647; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 1161 AAGAAGGCGAGCAGCAAGTCGTCTCTCTTCTTCAATGACGTCAACAGTGTGTCGAT 1220
 Db 657 AAGAAGGCGAGCAGCAAGTCGTCTCTCTTCTTCAATGACGTCAACAGTGTGTCGAT 598
 Qy 1221 GGTACTCTGTGGCAAGCAGGCGAGTCCCGTGTGAGAACTCTCAAGACCTTCTCCCTTT 1280
 Db 597 GGTACTCTGTGGCAAGCAGGCGAGTCCCGTGTGAGAACTCTCAAGACCTTCTCCCTTT 538
 Qy 1281 GCCTTTAACTTTTCTGAGTGATCTAGAGCCAGATTCATCTGCACAAATACGTGGTG 1340
 Db 537 GCCTTTAACTTTTCTGAGTGATCTAGAGCCAGATTCATCTGCACAAATACGTGGTG 478

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QY 1341 GTCTACTTTAGAGAGATTGATCAAAAGAGAGATTACAATGCTCTCAGTGTCTGCCCCAAG 1400
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Db 477 GTCTACTTTAGAGAGATTGATCAAAAGAGAGATTACAATGCTCTCAGTGTCTGCCCCAAG 418
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|
|
QY 1401 TACCATTTCATGAAGATGCCACTGCTTCTCTGTGAGAGACTTCTCATGTCAAGAGAGAG 1460
|
|
|
Db 417 TACCACCTCATGAAGATGCCACTGCTTCTCTGTGAGAGACTTCTCATGTCAAGAGAGAG 358
|
|
|
QY 1461 GTGTGACAGAGAAAGATGACAAAGCTGCGACAGTGGCTGCTCTCTTTGTAGCCACC 1520
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|
|
Db 357 GTGTGACAGAGAAAGATGACAAAGCTGCGACAGTGGCTGCTCTCTTTGTAGCCACC 298
|
|
|
QY 1521 CATGAGAAGCAAGAGACCTTTAAAGGCTTCTATCCACCAATTTACAGGG-AAAAAAGCTG 1579
|
|
|
Db 297 CATGAGAAGCAAGAGACCTTTAAAGGCTTCTATCCCAATTTACAGGGGAAAAAAGCTG 238
|
|
|
QY 1580 TGATGATCTGAAGCTTACTATGACGCTTACAAAGAGCTTAGTAATTTAAACATTTTAT 1639
|
|
|
Db 237 TGATGATCTGAAGCTTACTATGACGCTTACAAAGAGCTTAGTAATTTAAACATTTTAT 178
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|
|
QY 1640 ACCAATAAAATTTTCAAAATTTACTAACTAACTAGTACATTTAACTACAGATTGGAACACTAC 1699
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|
|
Db 177 ACCAATAAAATTTTCAAAATTTCTAACTAACTAGTACATTTAACTACAGATTGGAACACTAC 118
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|
QY 1700 ATTACAACCTTCAAAGCTGTTTATACATAGAAATCAATTTACAGCTTTTAAATGAAAACTG 1759
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Db 117 ATTACAACCTTCAAAGCTGTTTATACATAGAAATCAATTTACAGCTTTTAAATGAAAACTG 58
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QY 1760 TAACCAATTTGATAATGCAACAAATGAAGATCTTCCAAAAAAGAAAAAAGAAAAA 1816
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Db 57 TAACCAATTTGATAATGCAACAAATGAAGATCTTCCAAAAAAGAAAAAAGAAAAAAGAAAAA 1
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RESULT 7
AV727345 676 bp mRNA linear EST 17-OCT-2000
LOCUS AV727345 HTC Homo sapiens cDNA clone HTCACC09 5', mRNA sequence.
DEFINITION AV727345
ACCESSION AV727345
VERSION AV727345.1 GI:10836766
KEYWORDS EST.
SOURCE human.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 676)
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```
AUTHORS Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu
S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z., and Han,Z.
Homo sapiens cDNA HTC clones
```

```
TITLE Homo sapiens cDNA HTC clones
JOURNAL Unpublished (2000)
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```
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..676
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTCACC09"
/clone_lib="HTC"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
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FEATURES
source
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BASE COUNT 190 a 162 c 155 g 169 t
ORIGIN
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Query Match 34.4%; Score 628; DB 10; Length 676;
Best Local Similarity 96.9%; Pred. No. 1.4e-98;
Matches 651; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
QY 435 GCAATATATGAATGAAGATGGCCCTTCCATGCTGTGTGAATTTTCCCTCACCAGGCTGCCTA 494
|
|
|
Db 1 GCAATATATGAATGAAGATGGCCCTTCCATGCTGTGTGAATTTTCCCTCACCAGGCTGCCTA 60
|
|
|
QY 495 GACCACATAATGAATATAAAAAAAGTGTGTCAAGGCCGGAAGCTCTGGGATCCGAAC 554
|
|
|
Db 61 GACCACATAATGAATATAAAAAAAGTGTGTCAAGGCCGGAAGCTCTGGGATCCGAAC 120
|
|
|
QY 555 ATCACTGCTTGTAGAAGAAATGAGGAGACAGTAGAAGTGAATTCACAAACCACTCCCTG 614
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|
|
Db 121 ATCACTGCTTGTAGAAGAAATGAGGAGACAGTAGAAGTGAATTCACAAACCACTCCCTG 180
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QY 615 GGAAACAGATACATGGCTCTTTATCCAAACACAGCACTATCATCGGGTTTTCTCAGGTGTT 674
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Db 181 GGAAACAGATACATGGCTCTTTATCCAAACACAGCACTATCATCGGGTTTTCTCAGGTGTT 240
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|
|
QY 675 GAGCCACACCAAGAGAAACAAACGCGAGCTTCAGTGGTGAATTCACAGTCACTGGGGATAGT 734
|
|
|
Db 241 GAGCCACACCAAGAGAAACAAACGCGAGCTTCAGTGGTGAATTCACAGTCACTGGGGATAGT 300
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|
|
QY 735 GAAGGTGCTACGGTGACGCTGACTCCATATTTTCTTCTGTCGAGCACTGCATCCGA 794
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|
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Db 301 GAAGGTGCTACGGTGACGCTGACTCCATATTTTCTTCTGTCGAGCACTGCATCCGA 360
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|
QY 795 CATAAAGGAACAGTTGCTCTGTGCCCAACAAACAGCGTCCCTTTCCCTCTGGATTAACAAAC 854
|
|
|
Db 361 CATAAAGGAACAGTTGCTCTGTGCCCAACAAACAGCGTCCCTTTCCCTCTGGATTAACAAAC 420
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|
|
QY 855 AAAAGCAAGCCGGAGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 914
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|
|
Db 421 AAAAGCAAGCCGGAGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
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|
|
QY 915 GTGCTGTGGGAGGATCTATCTAATGTGAGGACGACGAAAGGATCAAGAAGACTTCTCTTT 974
|
|
|
Db 481 GTGCTGTGGGAGGATCTATCTAATGTGAGGACGACGAAAGGATCAAGAAGACTTCTCTTT 540
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|
QY 975 TCTACCACCACTACTGCCCCCCCATTAAGTCTTGTGGTTTACCATCTGAATATGT 1034
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|
|
Db 541 TTTTACCACCACTACTGCTCTCCCATTAAGATCTTGTGGTTTATCCATCTGAATATGT 600
|
|
|
QY 1035 TTCCATCACACAAATTTTACTTCACTGAATTTCTTCAAAACCAATTGCAGAAAGTGAAGTC 1094
|
|
|
Db 601 TTCCATCACACAAATTTTACTTCACTGAATTTCTTCAAAACCAATTGCAGAAAGTGAAGTC 659
|
|
|
QY 1095 ATCCTTGAAGAG 1106
|
|
|
Db 660 ACTCTTGAAGAG 671
|
|
|
RESULT 8
BE539514 641 bp mRNA linear EST 09-AUG-2000
LOCUS BE539514
DEFINITION 601060209F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3446667 5',
mRNA sequence.
ACCESSION BE539514
VERSION BE539514.1 GI:9768159
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 641)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
```

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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8419 row: a column: 04
High quality sequence stop: 639.
Location/Qualifiers
1. .841
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3446667"
/clone_lib="NIH MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
206 a 1152 g 165 t
BASE COUNT

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BASE COUNT	206 a	152 c	118 g	165 t
ORIGIN				
Query Match	34.0%;	Score 621.6;	DB 10;	Length 641;
Best Local Similarity	99.2%;	Pred. No. 1.8e-97;		
Matches 635; Conservative 0; Mismatches 4; Indels 1; Gaps 17				
Qy 1155	ACTCAAAGAAGGCGACGACAGCAAAAGTCGTCTTCCCTTTCTTTCCAATGACGCTCAACAGTG TG	1214		
Dd 1	ACTCAAAGAAGGCGACGACAGCAAAAGTCGTCTTCCCTTTCTTTCCAATGACGCTCAACAGTG TG	60		
Qy 1215	TGCGATGTACTGTGGCAAGAGCGAGGCGAGTCCCAGGTGAACCTCTCAAGACCTCTTC	1274		
Dd 61	TGCGATGTACTGTGGCAAGAGCGAGGCGAGTCCCAGGTGAACCTCTCAAGACCTCTTC	120		
Qy 1275	CCCCCTGCCTTAACCTTTTCGAGTGAATCTAAGAAGCGAGATTTCATCTGCACAATAAC	1334		
Dd 121	CCCCCTGCCTTTAACCTTTTCGAGTGAATCTAAGAAGCGAGATTTCATCTGCACAATAAC	180		
Qy 1335	GTGTGTGCTACTTTTAGAGAGATTGATACAAAAGCAGATTACAAATGCTCTCAGTGTCTGC	1394		
Dd 181	GTGTGTGCTACTTTTAGAGAGATTGATACAAAAGCAGATTACAGTGTCTCAGTGTCTGC	240		
Qy 1395	CCCCAAGTACCACCTTCATCAAGAGTGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCCAAG	1454		
Dd 241	CCCCAAGTACCACCTTCATCAAGAGTGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCCAAG	300		
Qy 1455	CAGCAGGTGTGAGCAGGAAAAAGATCACAAAGCTGCCACGATGCCAGTGGCTGCTCTTTGTAG	1514		
Dd 301	CAGCAGGTGTGAGCAGGAAAAAGATCACAAAGCTGCCACGATGCCAGTGGCTGCTCTTTGTAG	360		
Qy 1515	CCCAACCATGAGACGACGACGACCTTAAAGGCTTCTATCCACCAATTCAGGGAAAAA	1574		
Dd 361	CCCAACCATGAGACGACGACGACCTTAAAGGCTTCTATCCACCAATTCAGGGAAAAA	420		
Qy 1575	ACGTGTGATGATCCTGAAGCTTACTATGCAGCTPACAAACAGCCCTAGTAAATTAAGCAT	1634		
Dd 421	ACGTGTGATGATCCTGAAGCTTACTATGCAGCTPACAAACAGCCCTAGTAAATTAAGCAT	480		
Qy 1635	TTTTATACCAATAAAATTTTCAAATATTAATACTAACTAGCATTTAACTAACGATTGGAA	1694		
Dd 481	TTTTATACCAATAAAATTTTCAAATA-TGCTAACTAAATGTAGCATTTAACTAACGATTGGAA	539		
Qy 1695	ACTACATTTTCAACTTCAAGCTGTTTATACATAGAAATCAATTTACAGCTTTTAATTGAA	1754		
Dd 540	ACTACATTTTCAACTTCAAGCTGTTTATACATAGAAATCAATTTACAGCTTTTAATTGAA	599		
Qy 1755	AACGTGAACCAATTTTGATAATGCAACAATAAAGCATCTTC	1794		
Dd 600	AACGTGAACCAATTTTGATAATGCAACAATAAAGCATCTTC	639		

RESULT 9

BI458542	ACCESSION	REFERENCE
LOCUS	VERSION	AUTHOR
DEFINITION	KEYWORDS	TITLE
	SOURCE	JOURNAL
	ORGANISM	COMMENT

/note="Organ; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 kb. Library prepared by Life
Technologies."

BASE COUNT	206 a	152 c	118 q	165 t
recimologies.				

Query Match 34.0%; Score 621.6; DB 10; Length 641;
Best Local Similarity 99.2%; Pred. No. 1.8e-97;
Matches 635; Conservative 0; Mismatches 4; Indels 1;

Qy	1155	ACTCAAAGAAGGAGCAGACAAAGTCGTCTCTCTTTTCCAATGACGTCAACAGTGTG	1214
Db	1	ACTCAAAGAAGGAGCAGACAAAGTCGTCTCTCTTTTCCAATGACGTCAACAGTGTG	60
Qy	1215	TGCGATGGTACCTGTGGCAAGACGAGGAGCGAGTCCCAGTGAGAACTCTCAAGACCTCTTC	1274
Db	61	TGCGATGGTACCTGTGGCAAGACGAGGAGCGAGTCCCAGTGAGAACTCTCAAGACCTCTTC	120
Qy	1275	CCCTTTGCCTTTTAACTTTTCTGAGTGAATCTAAGAAAGCCAGATTCACTCTGCACAAATAC	1334
Db	121	CCCTTTGCCTTTTAACTTTTCTGAGTGAATCTAAGAAAGCCAGATTCACTCTGCACAAATAC	180
Qy	1335	GTGGTGTCTACTTTTAGAGAGATTGATCAAAAGACGATTACAAATGCTCTCAGTGTCTGC	1394
Db	181	GTGGTGTCTACTTTTAGAGAGATTGATCAAAAGACGATTACAGTGTCTCTCAGTGTCTGC	240
Qy	1395	CCCAAGTACCACTTCATGAAGGATGCCACTGTCTTTCTGTGCAGAACTTCTCCATGTCAAG	1454
Db	241	CCCAAGTACCACTTCATGAAGGATGCCACTGTCTTTCTGTGCAGAACTTCTCCATGTCAAG	300

Qy	1455	CAGCAGGTGTCAGCAGGAAAAAGATCACAAAGCCTGCCAGATGGCTGCTGCTCTTGTAG	1514
Db	301	CAGCAGGTGTCAGCAGGAAAAAGATCACAAAGCCTGCCAGATGGCGCTGCTCTTGTAG	360
Qy	1515	CCACCCATGAGAGCAAGAGACCTTAAAGGCTTCCATCCCAACAATTACAGGAAAAA	1574
Db	361	CCACCCATGAGAGCAAGAGACCTTAAAGGCTTCCATCCCAACAATTACAGGAAAAA	420
Qy	1575	ACGTGTGATGATCCTCAAGCTTACTATGCAGGCTTACAACAGCCTTAGTAATTAAAAACAT	1634
Db	421	ACGTGTGATGATCCTGAAGCTTACTATGCAGGCTTACAACAGCCTTAGTAATTAAAAACAT	480
Qy	1635	TTTATACCAATAAAATTTTCAAATATTACTAACTAATGTAGCAITTAACACGATTGGAA	1694
Db	481	TTTATACCAATAAAATTTTCAAATA-TGCTAACTAATGTAGCATTTACTACGATTGGAA	539
Qy	1695	ACTACATTTACAACTTCAAAGCTGTTTTATACATAGAATAAATCAATTACAGCTTTTAATTGAA	1754
Db	540	ACTACATTTACAACTTCAAAGCTGTTTTATACATAGAATAAATCAATTACAGCTTTTAATTGAA	599
Qy	1755	AACGTGTAACCAATTTTGATTAATGCACAATAAAGAATCTTTC	1794
Db	600	AACGTGAACCAATTTTGATTAATGCACAATAAAGAATCTTTC	639

RESULT 9

BI458542	788 bp	mrna	linear	EST 21-AUG-2001		
LOCUS	603138643F1 NIH_MGC_96	homo sapiens	cdna clone	IMAGE:5278067 5',		
DEFINITION	mRNA sequence.					
ACCESSION	BI458542					
VERSION	BI458542.1	GI:15249198				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
TITLE	1 (bases 1 to 788)					
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .					
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)					
	Unpublished (1999)					
	Contact: Robert Strausberg, Ph.D.					
	Email: cgabbs-r@mail.nih.gov					
	Tissue Procurement: Miklos Palkovits, M.D., Ph.D.					
	cdna Library Preparation: Michael J. Brownstein (NHGRI), Shiraki					
	Toshiyuki and Piero Carninci (RIKEN)					
	cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)					
	DNA Sequencing by: Incyte Genomics, Inc.					
	Clone distribution: MGC clone distribution information can be					
	found through the I.M.A.G.E. Consortium/LLNL at:					
	http://image.llnl.gov					
	Plate: LLAM11702	row: e	column: 12			
	High quality sequence stop: 784.					

FEATURES
source

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1. 788
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/db_xref="taxon:9606"
/clone="IMAGE:5278067"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
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BASE COUNT
196 a 206 c 201 g 184 t 1 others
/root/Note/Brain/Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTWN-3',
size-selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH MGC Library."
196 a 206 c 201 g 184 t 1 others

BASE COUNT	19
ORIGIN	

Query Match 33.4%; Score 610.4; DB 13; Length 788;
Best Local Similarity 98.9%; Pred. No. 1.4e-95;
Matches 656; Conservative 0; Mismatches 2; Indels 5; Gaps 4;

Qy	360	TGACATATTTTCTATATCGCTTCCCTGTAGAGCTGAACACAGTCTATTTCATTTGGGGC	419
Db	130	TGACATATTTTCTATATCGCTTCCCTGTAGAGCTGAACACAGTCTATTTCATTTGGGGC	189
Qy	420	CATAATATTCCTAATCGAATATGAATGAAGATGGCCCTTCATGCTCTGGAATTCAC	479
Db	190	CATAATATTCCTAATCGAATATGAATGAAGATGGCCCTTCATGCTCTGGAATTCAC	249
Qy	480	TCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAAGTGTCTCAAGCCCGGAAGC	539
Db	250	TCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAAGTGTCTCAAGCCCGGAAGC	309
Qy	540	CTGTGGGATCCGAACATCACTGTTGTATAGAGAATAGGAGACAGTAGAAGTGAATTC	599
Db	310	CTGTGGGATCCGAACATCACTGTTGTATAGAGAATAGGAGACAGTAGAAGTGAATTC	369
Qy	600	ACAACCACTCCCTGGGAACAGATACATGGCTTTATCCACACAGCACTATCATCGG	659
Db	370	ACAACCACTCCCTGGGAACAGATACATGGCTTTATCCACACAGCACTATCATCGG	427
Qy	660	TTTTCTCAGTGTGTCAGCCACACCGAGAGAAACAAACCGAGCTTCAGTGTGATTC	719

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Db 428 TTTTCTCAGGTGTTTGAGCCACACCAAGAAACAAACGCGAGCTTCAGTGGTGAATCCA 487
QY 720 GTGACTGGGGATAGTGAAGTGCTACGGTGCAGCTGACTGCATATATTTTCTACTTGTGGC 779
Db 488 GTGACTGGGGATAGTGAAGTGCTACGGTGCAGCTGACTGCATATATTTTCTACTTGTGGC 547
QY 780 AGCGACTGCATCCGACATAAAGAAACAGTTGTCTCTGCCCAACAAACAGCGCGTCCCTTTC 839
Db 548 AGCGACTGCATCCGACATAAAGAAACAGTTGTCTCTGCCCAACAAACAGCGCGTCCCTTTC 607
QY 840 CTTCTCGATAACAAACAAAGCAAGCGGAGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTG 899
Db 608 CTTCTCGATAACAAACAAAGCAAGCGGAGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTG 667
QY 900 CTGGTGGCCACA-TGGGTGCTGTGGCAGGATCTATCTAATGTGAGCAGCAAGAGGAT 958
Db 668 CTGGTGGCACAATTGGGTGCTGTGGCAGGATCTATCTAATGTGAGCAGCAAGAGGAT 727
QY 959 CAAGAAGACTTCTCTTCTACCAACACACTACTGCCCCCAATTAAGTTCTTGTGGTTTA 1018
Db 728 C-AGAAGACTTCTCTTCTTACCACACA-TACTGCCCCCAATTAAGTTCTTGTGGTTTA 785
QY 1019 CCC 1021
Db 786 CCC 788

RESULT 10
BG433769/c
LOCUS
DEFINITION 60249774F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4611491 5',
mRNA sequence.
ACCESSION BG433769
VERSION BG433769.1 GI:13340275
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 630)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW1358 row: g column: 12
High quality sequence stop: 610.
Location/Qualifiers
1. .630
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_75"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCATAGAGCGGAGCGGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
170 a 111 c 149 g 200 t

BASE COUNT
ORIGIN

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Query Match 32.7%; Score 598.2; DB 12; Length 630;
Best Local Similarity 97.9%; Pred. No. 1.9e-93;
Matches 606; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1185 TTCCTCTCTTCCAAATGACGTCAACAGTGTGTGCGATGATGCTGTGGCAAGAGCGAGGCG 1244
Db 626 TCCTTCTCTTCCAAATGACGTCAACAGTGTGTGCGATGATGCTGTGGCAAGAGCGAGGCG 567
QY 1245 AGTCCAGTGAAGACTCTCAAGACCTCTTCCCTTGGCTTTAACTTTCTGCGAGTGAT 1304
Db 566 AGTCCAGTGAAGACTCTCAAGACCTCTTCCCTTGGCTTTAACTTTCTGCGAGTGAT 507
QY 1305 CTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGGTCTTACTTTAGAGAGATTGATACA 1364
Db 506 CTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGGTCTTACTTTAGAGAGATTGATACA 447
QY 1365 AAAGACGATTCAATGTCTCAGTGTCTGCCCAAGTACCACTTTCATGAAGGATGCCACT 1424
Db 446 AAAGACGATTCAATGTCTCAGTGTCTGCCCAAGTACCACTTTCATGAAGGATGCCACT 387
QY 1425 GCTTTCTGTGAGAACTTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAAGATCACA 1484
Db 386 GCTTTCTGTGAGAACTTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAAGATCACA 327
QY 1485 GCTGCCACGATGGCTGCTGCTCTTGTAGCCACCCATGAGAACCAAGAGACCTTTAAAG 1544
Db 326 GCTGCCACGATGGCTGCTGCTCTTGTAGCCACCCATGAGAACCAAGAGACCTTTAAAG 267
QY 1545 GCTTCTTATCCCAACAAATTACAGGAAAAAAACGTGTGATGATCTTGAAGCTTTACTATCA 1604
Db 266 GCTTCTTATCCCAACAAATTACAGGAAAAAAACGTGTGATGATCTTGAAGCTTTACTATCA 207
QY 1605 GCCTACAAACAGCCTTAGTAATTAACACATTTTATACCAATARAATTTTCAATATTACT 1664
Db 206 GCCTACAAACAGCCTTAGTAATTAACACATTTTATACCAATARAATTTTCAATATTACT 147
QY 1665 AACTAATGTAGCATTAACTAAGATTGAAAACTACATTATCAAACTTTCAAAGCTGTTTAT 1724
Db 146 AACTAATGTAGCATTAACTAAGATTGAAAACTACATTATCAAACTTTCAAAGCTGTTTAT 87
QY 1725 ACATAGAAATCAATTACAGCTTTTAATTCGAAAACTGTAACTTTGATAATGCAACAATA 1784
Db 86 ACATAGAAATCAATTACAGCTTTTAATTCGAAAACTGTAACTTTGATAATGCAACAATA 27
QY 1785 AAGCATCTTCCAAAAAAA 1803
Db 26 AAGCATCTTCCAAAAACA 8

RESULT 11
BG433769
LOCUS
DEFINITION 603244108F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5286745 5',
mRNA sequence.
ACCESSION BG433769
VERSION BG433769.1 GI:15495122
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 842)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

```


from a pool of 5,000 clones made from the same library (cloneIDs 132376-132391, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT	137 a	85 c	115 g	173 t
ORIGIN				
Query Match	27.2%	Score 497;	DB 10;	Length 510;
Best Local Similarity	99.0%	Pred. No. 5.3e-76;		
Mismatches	500;	Conservative	0;	Mismatches 5;
			Indels	0;
			Gaps	0;

QY 1290 CTTTCTGAGTATAGAGCCAGATTCTCTGCACAAATAGCTGTGCTACTTTT 1349
 |||||
 Db 510 CTTTCTGAGTATAGAGCCAGATTCTCTGCACAAATAGCTGTGCTACTTT 451
 |||||
 QY 1350 AGAGAGATTGATACAAAGACGATTACAATGTCTCAGTGTCTGCCCAAGTACCACTTC 1409
 |||||
 Db 450 AGAGAGATTGATACAAAGACGATTACAATGTCTCAGTGTCTGCCCAAGTACCACTTC 391
 |||||
 QY 1410 ATGAGGATGCCACTGCTTTCTGTGAGAACCTTCTCCATGTCAAGCAGAGGTGTGAGCA 1469
 |||||
 Db 390 ATGAGGATGCCACTGCTTTCTGTGAGAACCTTCTCCATGTCAAGCAGAGGTGTGAGCA 331
 |||||
 QY 1470 GGAAGAGATCAAGCCTGCCAGATGCTGTCTCTGTAGCCACCCATGAGAG 1529
 |||||
 Db 330 GGAAGAGATCAAGCCTGCCAGATGCTGTCTCTGTAGCCACCCATGAGAG 271
 |||||
 QY 1530 CAAGAGACCTTAAAGCTTCTTATCCCAATTTACAGGGAACAAACGTGTGATGATCT 1589
 |||||
 Db 270 CAAGAGACCTTAAAGCTTCTTATCCCAATTTACAGGGAACAAACGTGTGATGATCT 211
 |||||
 QY 1590 GAAGCTTACTGACGCTTACAAACAGCCTTAGTAAATTAACATTTTATACCAATAAAA 1649
 |||||
 Db 210 GAAGCTTACTGACGCTTACAAACAGCCTTAGTAAATTAACATTTTATACCAATAAAA 151
 |||||
 QY 1650 TTTTCAATTAATTAAGTAACTAGTAACTAGTAACTAGTAACTAGTAACTAGTAACT 1709
 |||||
 Db 150 TTTTCAATTAATTAAGTAACTAGTAACTAGTAACTAGTAACTAGTAACTAGTAACT 91
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 QY 1710 TCAAGCTGTTTTATACATAGAAATCAATTAAGCTTTAAATTAAGCTTTAACTAACTTTT 1769
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 Db 90 TCAAGCTGTTTTATACATAGAAATCAATTAAGCTTTAAATTAAGCTTTAACTAACTTTT 31
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 QY 1770 GATAATGCAACATAAAGCATCTTC 1794
 |||||
 Db 30 GATAATGCAACATAAAGCATCTTC 6
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RESULT 15
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 LOCUS
 DEFINITION 7n36f01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3566736 3',
 mRNA sequence.
 ACCESSION BF110326
 VERSION BF110326.1 GI:10940016
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 509)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E.B. Consortium/LLNL, send email to: info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 470.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:3566736"
 /clone_lib="NCI_CGAP_Lu24"
 /tissue_type="carcinoid"
 /lab_host="DH10B"
 /note="Organ: lung; Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT	132 a	84 c	113 g	180 t
ORIGIN				
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Best Local Similarity	98.0%	Pred. No. 2.6e-75;		
Mismatches	499;	Conservative	0;	Mismatches 10;
			Indels	0;
			Gaps	0;

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 |||||
 Db 509 GCAGTGATCTAGAGCCAGATTCTCTGCACAAATAGCTGTGCTACTTTAGAGAGA 450
 |||||
 QY 1357 TTGATACAAAGACGATTACAATGTCTCAGTGTCTGCCCAAGTACCACTTCATGAAGG 1416
 |||||
 Db 449 TTGATACAAAGACGATTACAATGTCTCAGTGTCTGCCCAAGTACCACTTCATGAAGG 390
 |||||
 QY 1417 ATGCCACTGCTTTCTGTGAGAACCTTCCATGTCAAGCAGAGGTGTGAGAGAGAG 1476
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 Db 389 ATGCCACTGCTTTCTGTGAGAACCTTCCATGTCAAGCAGAGGTGTGAGAGAGAG 330
 |||||
 QY 1477 GATCACAGCCTGCCAGCAGTGTCTCTCTGTAGCCACCCATGAGAGAGAGAGAGA 1536
 |||||
 Db 329 GATCACAGCCTGCCAGCAGTGTCTCTCTGTAGCCACCCATGAGAGAGAGAGAGA 270
 |||||
 QY 1537 CCTTAAAGCTTCTCTATCCCAATTTACAGGGAACAAACGTGTGATGATCTCTGAAGCTT 1596
 |||||
 Db 269 CCTTAAAGCTTCTCTATCCCAATTTACAGGGAACAAACGTGTGATGATCTCTGAAGCTT 210
 |||||
 QY 1597 ACTATGCAGCCTTACAAACAGCCTTAGTAAATTAACATTTTATACCAATAAAATTTCAA 1656
 |||||
 Db 209 ACTATGCAGCCTTACAAACAGCCTTAGTAAATTAACATTTTATACCAATAAAATTTCAA 150
 |||||
 QY 1657 ATATTACTAACTAACTAGTACGATTAACTAAGTAACTAAGTAACTAAGTAACTAAGT 1716
 |||||
 Db 149 ATATTGCTAACTAACTAGTACGATTAACTAAGTAACTAAGTAACTAAGTAACTAAGT 90
 |||||
 QY 1717 TGTTTTATACATAGAAATCAATTTACAGCTTTAAATTAAGAACTGTAACTAATTTGATAATG 1776
 |||||
 Db 89 TGTTTTATACATAGAAATCAATTTACAGCTTTAAATTAAGAACTGTAACTAATTTGATAATG 30
 |||||
 QY 1777 CAACAATAAGCATCTTCCAAAAA 1805
 |||||
 Db 29 CAACAATAAGCATCTTCCAAAAA 1

Search completed: May 28, 2003, 10:12:39
 Job time : 2569.08 secs

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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 23:34:39 ; Search time 204.956 Seconds
(without alignments)
11770.723 Million cell updates/sec

Title: US-09-778-971-1
Perfect score: 1827
Sequence: 1 cggcgatgctgctgctgctg.....aaaaaaaaaaaaaaaaaaaaa 1827

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues
Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications NA.*
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
 - 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
 - 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
 - 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
 - 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
 - 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
 - 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
 - 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
 - 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
 - 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
 - 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
 - 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1827	100.0	1827	10	US-09-778-971-1
2	1786	97.8	1841	10	US-09-886-404-17
3	1785.6	97.7	1796	9	US-09-863-818A-1
4	1552.4	85.0	2015	10	US-09-886-404-19
5	1509.2	82.6	1515	9	US-09-874-503-11
6	1509.2	82.6	1515	9	US-10-000-157-11
7	1509.2	82.6	1515	9	US-10-063-547-157
8	1509.2	82.6	1515	9	US-09-747-259-11
9	1509.2	82.6	1515	9	US-10-174-590-399
10	1509.2	82.6	1515	9	US-10-176-758-399
11	1509.2	82.6	1515	9	US-10-063-616-157
12	1509.2	82.6	1515	9	US-10-175-737-399
13	1509.2	82.6	1515	9	US-10-063-502-157
14	1509.2	82.6	1515	9	US-10-173-706-399
15	1509.2	82.6	1515	9	US-10-176-738-399
16	1509.2	82.6	1515	9	US-10-175-752-399
17	1509.2	82.6	1515	9	US-10-176-482-399
18	1509.2	82.6	1515	9	US-10-176-757-399
19	1509.2	82.6	1515	9	US-10-176-913-399

20	1509.2	82.6	1515	9	US-10-180-552-399	Sequence 399, App
21	1509.2	82.6	1515	9	US-10-180-557-399	Sequence 399, App
22	1509.2	82.6	1515	9	US-10-173-700-399	Sequence 399, App
23	1509.2	82.6	1515	9	US-10-174-572-399	Sequence 399, App
24	1509.2	82.6	1515	9	US-10-174-579-399	Sequence 399, App
25	1509.2	82.6	1515	9	US-10-174-582-399	Sequence 399, App
26	1509.2	82.6	1515	9	US-10-174-588-399	Sequence 399, App
27	1509.2	82.6	1515	9	US-10-175-739-399	Sequence 399, App
28	1509.2	82.6	1515	9	US-10-175-740-399	Sequence 399, App
29	1509.2	82.6	1515	9	US-10-175-743-399	Sequence 399, App
30	1509.2	82.6	1515	9	US-10-176-488-399	Sequence 399, App
31	1509.2	82.6	1515	9	US-10-176-492-399	Sequence 399, App
32	1509.2	82.6	1515	9	US-10-176-747-399	Sequence 399, App
33	1509.2	82.6	1515	9	US-10-176-750-399	Sequence 399, App
34	1509.2	82.6	1515	9	US-10-176-985-399	Sequence 399, App
35	1509.2	82.6	1515	9	US-10-176-987-399	Sequence 399, App
36	1509.2	82.6	1515	9	US-10-176-991-399	Sequence 399, App
37	1509.2	82.6	1515	9	US-10-176-992-399	Sequence 399, App
38	1509.2	82.6	1515	9	US-10-176-993-399	Sequence 399, App
39	1509.2	82.6	1515	9	US-10-184-658-399	Sequence 399, App
40	1509.2	82.6	1515	9	US-10-173-695-399	Sequence 399, App
41	1509.2	82.6	1515	9	US-10-173-697-399	Sequence 399, App
42	1509.2	82.6	1515	9	US-10-173-705-399	Sequence 399, App
43	1509.2	82.6	1515	9	US-10-174-576-399	Sequence 399, App
44	1509.2	82.6	1515	9	US-10-174-585-399	Sequence 399, App
45	1509.2	82.6	1515	9	US-10-174-586-399	Sequence 399, App

ALIGNMENTS

RESULT 1
US-09-778-971-1
; Sequence 1, Application US/09778971
; Patent No. US20020102639A1
; GENERAL INFORMATION:
; APPLICANT: Shaughnessy, John D.
; TITLE OF INVENTION: EV127 Gene Sequence and Protein Encoded Thereby
; FILE REFERENCE: D6138
; CURRENT APPLICATION NUMBER: US/09/778,971
; PRIORITY FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/180,374
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 1
; LENGTH: 1827
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: prim transcript
; OTHER INFORMATION: cDNA of human EV127
US-09-778-971-1

Query Match	100.0%	Score 1827;	DB 10;	Length 1827;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1827;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CGGCGATGTCGCTCGTCTGCTGATAAGCCTGGCGCGCTGTGCAGGAGCGCGTACCCCGAG	60	
Db	1	CGGCGATGTCGCTCGTCTGCTGATAAGCCTGGCGCGCTGTGCAGGAGCGCGTACCCCGAG	60	
Qy	61	AGCCGACGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTTACAACATG	120	
Db	61	AGCCGACGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTTACAACATG	120	
Qy	121	ATCTAATCCCGGAGACTTGAGGACCTCCGAGTAGAACCTGTTACAACATGTTGCA	180	
Db	121	ATCTAATCCCGGAGACTTGAGGACCTCCGAGTAGAACCTGTTACAACATGTTGCA	180	
Qy	181	CAGGGGACTTCAATTTGATGAATGAAGTGGTACTCCGGGCAGATCCGACATCC	240	
Db	181	CAGGGGACTTCAATTTGATGAATGAAGTGGTACTCCGGGCAGATCCGACATCC	240	

Qy	241	GCTTGTGAAAGGCCACAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTCTACAGCT	300
Db	241	GCTTGTGAAAGGCCACAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTCTACAGCT	300
Qy	301	GTGTGAGGTGCAATTACACAGAGGCCCTTCCAGACTCAGACACTCAGACAGACCCCTCTGGTGGTAAAT	360
Db	301	GTGTGAGGTGCAATTACACAGAGGCCCTTCCAGACTCAGACACTCAGACAGACCCCTCTGGTGGTAAAT	360
Qy	361	GGACATTTTCTTATATCGGCTTCCCTGTAGAGCTGAAACAAGTCTTATTTCAATTCGGGGCCC	420
Db	361	GGACATTTTCTTATATCGGCTTCCCTGTAGAGCTGAAACAAGTCTTATTTCAATTCGGGGCCC	420
Qy	421	ATAATATTCCTAATGCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAAATTTCACTT	480
Db	421	ATAATATTCCTAATGCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAAATTTCACTT	480
Qy	481	CACGAGCTGCCTAGACCACATATGAAATATAAAAAAGTGTGTGAAGCCCGGAAGCC	540
Db	481	CACGAGCTGCCTAGACCACATATGAAATATAAAAAAGTGTGTGAAGCCCGGAAGCC	540
Qy	541	TGTGGGATCCGAACATCACCTGCTTGTGAAGAAGATGAGGAGACAGTAGAAGTGAATTTCA	600
Db	541	TGTGGGATCCGAACATCACCTGCTTGTGAAGAAGATGAGGAGACAGTAGAAGTGAATTTCA	600
Qy	601	CAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAAACAGACACTATCATCGGGT	660
Db	601	CAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAAACAGACACTATCATCGGGT	660
Qy	661	TTTCTCAGGTGTTTGAAGCCACACCAGAGAAACAAACGGGAGCTTCAGTGTGATTCAG	720
Db	661	TTTCTCAGGTGTTTGAAGCCACACCAGAGAAACAAACGGGAGCTTCAGTGTGATTCAG	720
Qy	721	TGACTGGGATAGTGAAGTGTCTACGGTGCAGCTGCATTCATATTTTCTACTTGTGGCA	780
Db	721	TGACTGGGATAGTGAAGTGTCTACGGTGCAGCTGCATTCATATTTTCTACTTGTGGCA	780
Qy	781	GCAGCTGCATCCGACATAAAGGAACAGTTGTGCTCTGGCCCAACAAAGGCGTCCCTTTTC	840
Db	781	GCAGCTGCATCCGACATAAAGGAACAGTTGTGCTCTGGCCCAACAAAGGCGTCCCTTTTC	840
Qy	841	CTCTGGATAAACAACAAAGAGCGGGAGGTGGCTGCCTCTCTCTGCTGTCTCTGC	900
Db	841	CTCTGGATAAACAACAAAGAGCGGGAGGTGGCTGCCTCTCTCTGCTGTCTCTGC	900
Qy	901	TGTTGGCCACATGGGTGCTGTGGCAGGATCTATCTAATGTGAGGACGAAAGGATCA	960
Db	901	TGTTGGCCACATGGGTGCTGTGGCAGGATCTATCTAATGTGAGGACGAAAGGATCA	960
Qy	961	AGAAGACTTCCTTTTCTACCAACACACTACTGCCCCCAATTAAGGTCTTGTGGTTTACC	1020
Db	961	AGAAGACTTCCTTTTCTACCAACACACTACTGCCCCCAATTAAGGTCTTGTGGTTTACC	1020
Qy	1021	CATCTGAAATATGTTTCCATFACACAATTTGTTACTTCACCTGAATTTCTCAAAACCATT	1080
Db	1021	CATCTGAAATATGTTTCCATFACACAATTTGTTACTTCACCTGAATTTCTCAAAACCATT	1080
Qy	1081	GCAGAGTGAGGTCACTCTGAAAGTGGCAGAAAGAAATAGCAGAGATGGTCCAG	1140
Db	1081	GCAGAGTGAGGTCACTCTGAAAGTGGCAGAAAGAAATAGCAGAGATGGTCCAG	1140
Qy	1141	TGCAGTGGCTTGGCATTCAAAAGAGGACAGACAAAGTGGTCTTCTCTTTTCCAATG	1200
Db	1141	TGCAGTGGCTTGGCATTCAAAAGAGGACAGACAAAGTGGTCTTCTCTTTTCCAATG	1200
Qy	1201	ACGTCAACAGTGTGCGATGGTACTGTGGCAGAGCGAGGGCAGTCCCAGTGAGAACT	1260
Db	1201	ACGTCAACAGTGTGCGATGGTACTGTGGCAGAGCGAGGGCAGTCCCAGTGAGAACT	1260
Qy	1261	CTCAGACCTCTTCCCCTTGGCTTTTAACTTTTCTGCAGTGTACTAAGAGCCAGATTC	1320
Db	1261	CTCAGACCTCTTCCCCTTGGCTTTTAACTTTTCTGCAGTGTACTAAGAGCCAGATTC	1320
Qy	1321	ATCTGCACAAATACGTGGTGGTCTACTTTTAGAGAGATTTGATACAAAAGACGATTTACAATG	1380

Db	1321	ATCTGCAAAATACGTGGTGTACTTTAGAGAGATTGATACAAAGACGATTACAAATG	1380
Qy	1381	CTCTCAGTGTCTCCCAAGTACCACCTTCATGAAGATGCCACTGCTTCTGTGCAGAAC	1440
Db	1381	CTCTCAGTGTCTCCCAAGTACCACCTTCATGAAGATGCCACTGCTTCTGTGCAGAAC	1440
Qy	1441	TTCTCCATGTCAAGCAGCAGGTGTGTCAGCAGGAAAAGATCAACAGCTGCCACGATGGCT	1500
Db	1441	TTCTCCATGTCAAGCAGCAGGTGTGTCAGCAGGAAAAGATCAACAGCTGCCACGATGGCT	1500
Qy	1501	GCTGCTCTTGTAGCCACCACCATGAGAGCAAGACCTTAAAGGCTTCTATCCACCA	1560
Db	1501	GCTGCTCTTGTAGCCACCACCATGAGAGCAAGACCTTAAAGGCTTCTATCCACCA	1560
Qy	1561	ATTACAGGGAAAAACGTGTGATGATCTCTGAAGCTTACTATGCAGCCTCAACACAGCCTT	1620
Db	1561	ATTACAGGGAAAAACGTGTGATGATCTCTGAAGCTTACTATGCAGCCTCAACACAGCCTT	1620
Qy	1621	AGTAATTTAAACATTTTTATACCAATAAAATTTTCAATATTTACTAACTAATGTAGCAATTA	1680
Db	1621	AGTAATTTAAACATTTTTATACCAATAAAATTTTCAATATTTACTAACTAATGTAGCAATTA	1680
Qy	1681	ACTACGATTTGGAACTACATTTTCAACTTCAGAGCTGTTTTATACATAGAAATCAATTA	1740
Db	1681	ACTACGATTTGGAACTACATTTTCAACTTCAGAGCTGTTTTATACATAGAAATCAATTA	1740
Qy	1741	CAGCTTTTAATTGAAAACTGTAACCACTTTTGATTAATGCAACAAATAAAGCATCTTCCAAAAA	1800
Db	1741	CAGCTTTTAATTGAAAACTGTAACCACTTTTGATTAATGCAACAAATAAAGCATCTTCCAAAAA	1800
Qy	1801	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1827
Db	1801	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1827

RESULT 2

US-09-886-404-17
; Sequence 17, Application US/09886404
; Patent No. US20020037524A1
; GENERAL INFORMATION:
; APPLICANT: Medlock, Eugene
; APPLICANT: Yeh, Richard
; APPLICANT: Silbiger, Scott M.
; APPLICANT: Elliot, Gary S.
; APPLICANT: Nguyen, Hung Q.
; APPLICANT: Jing, Shuqian
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/37128B
; CURRENT APPLICATION NUMBER: US/09/886,404
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/810,384
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/266,159
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,125
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 17
; LENGTH: 1841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(1555)
US-09-886-404-17

Query Match	97.8%	Score 1786;	DB 10;	Length 1841;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 1789;	Conservative	0;	Mismatches 5;	Indels 0;
Gaps	0;			
Ov	1	CGGGGATGTCGTGCTGTATAGACCTGCGCGGCTGTGCAGGAGCGCCGTACCCCGAG	60	

Db	1125	GCAGAAGTGAGGTCACTCTCGAAAAAGTGGCGAAGAAAGAAATATAGCAGAGATGGGTCCAG	11184
Qy	1141	TGCAGTGGCTTGGCACTCAAAAAGAGGAGCAGACAAAGTCGTCTTCCCTCTTTTCCAATG	1200
Db	1185	TGCAGTGGCTTGGCACTCAAAAAGAGGAGCAGACAAAGTCGTCTTCCCTCTTTCCAATG	1244
Qy	1201	ACGTCAACAGTGTGCGATGTGATCTGTGGCAAGAGCGAGGCGAGTCCCAAGTCAGNACT	1260
Db	1245	ACGTCAACAGTGTGCGATGTGATCTGTGGCAAGAGCGAGGCGAGTCCCAAGTCAGNACT	1304
Qy	1261	CTCAAGACCTCTTCCGCCCTTGCCTTTAACTTTTCTGCAGTGTATCAAGAGCCAGATTC	1320
Db	1305	CTCAAGACCTCTTCCGCCCTTGCCTTTAACTTTTCTGCAGTGTATCAAGAGCCAGATTC	1364
Qy	1321	ATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGTATCAAAAGACGATTACAATG	1380
Db	1365	ATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGTATCAAAAGACGATTACAATG	1424
Qy	1381	CTCTCAGTGTCTGCCCCCAAGTACCACCTTCATGAAGAGTGCCACCTGCTTTCTGTGCAGAAC	1440
Db	1425	CTCTCAGTGTCTGCCCCCAAGTACCACCTTCATGAAGAGTGCCACCTGCTTTCTGTGCAGAAC	1484
Qy	1441	TTCTCAGTGTCAAGCAGCAGGTGTGCAGCAGGAAAAGATCAACAGCCTGCCACGATGGCT	1500
Db	1485	TTCTCAGTGTCAAGCAGCAGGTGTGCAGCAGGAAAAGATCAACAGCCTGCCACGATGGCT	1544
Qy	1501	GCTGCTCTCTGTAGCCACCCTCATGATGAGACGAGACCTTAAAGGCTTCCTATCCACCA	1560
Db	1545	GCTGCTCTCTGTAGCCACCCTCATGATGAGACGAGACCTTAAAGGCTTCCTATCCACCA	1604
Qy	1561	ATTACAGGGAAAAACGTTGTATGATCTCTGAAGCTTACTATGCAGCCTCAAAACAGCCTT	1620
Db	1605	ATTACAGGGAAAAACGTTGTATGATCTCTGAAGCTTACTATGCAGCCTCAAAACAGCCTT	1664
Qy	1621	ACTAAATTAAACATTTTATACCAATAAAATTTTCAAAATTTACTAACTAATGTAGCAATTA	1680
Db	1665	AGTAAATTAAACATTTTATACCAATAAAATTTTCAAAATTTTGCCTAATGTAGCAATTA	1724
Qy	1681	ACTAACGATTGAAACATCAATTTACAACCTTCAAAGCTGTGTTTTATACATAGAAATCAATTA	1740
Db	1725	ACTAACGATTGAAACATCAATTTACAACCTTCAAAGCTGTGTTTTATACATAGAAATCAATTA	1784
Qy	1741	CAGCTTTAATTGAAACATGTACCAATTTTGTATATGCAACAAATAAAGCATCTTC	1794
Db	1785	CAGCTTTAATTGAAACATGTACCAATTTTGTATATGCAACAAATAAAGCATCTTC	1838

METHODS

Query Match		97.7%	Score 1785.6	DB 9	Length 1796	
Best Local Similarity		99.8%	Pred. No. 0			
Matches 1788		Conservative	0	Mismatches	4	Indels 0; Gaps 0;
Qy	3	GCGATGTCGCTCGCTGATGAAGCCCTGCGCGCGCTGTCAGGAGCGCGTACCCCGAGAG	62			
Db	1	GCGATGTCGCTCGCTGCTGAAGCCCTGCGCGCGCTGTCAGGAGCGCGTACCCCGAGAG	60			
Qy	63	CCGACCGCTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGATGGATGCTTACAACATGAT	122			
Db	61	CCGACCGCTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGATGGATGCTTACAACATGAT	120			
Qy	123	CTAATCCCGGAGACTTGAAGGACCTCCGAGTAGAACTCTGTTTAACTAGTGTGCAACA	182			
Db	121	CTAATCCCGGAGACTTGAAGGACCTCCGAGTAGAACTCTGTTTAACTAGTGTGCAACA	180			
Qy	183	GGGACTATTCAATTTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT	242			
Db	181	GGGACTATTCAATTTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT	240			
Qy	243	TTGTGAAGCCCAACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTTACAGCTGT	302			
Db	241	TTGTGAAGCCCAACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTTACAGCTGT	300			
Qy	303	GTGAGTGCATTTACACAGAGGCTTCCAGACTCAGACCCCTCTGCTGTTAAATGG	362			
Db	301	GTGAGTGCATTTACACAGAGGCTTCCAGACTCAGACCCCTCTGCTGTTAAATGG	360			
Qy	363	ACATTTTCTATATCGGCTTCCCTGTAGAGTGAACACAGTCTATTTTCAATGGGGCCAT	422			
Db	361	ACATTTTCTATATCGGCTTCCCTGTAGAGTGAACACAGTCTATTTTCAATGGGGCCAT	420			
Qy	423	AATATTCTTAAATCAATATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT	482			
Db	421	AATATTCTTAAATCAATATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT	480			
Qy	483	CCAGGTGCTTAGACCAATATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT	542			
Db	481	CCAGGTGCTTAGACCAATATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT	540			
Qy	543	TGGATCCGAACTACTGCTGTAGAGAGATGAGGAGACAGTGAAGTGAATTCACCTCA	602			
Db	541	TGGATCCGAACTACTGCTGTAGAGAGATGAGGAGACAGTGAAGTGAATTCACCTCA	600			
Qy	603	ACCACTCCCTCGGAAACAGATACATGGCTCTTATCCAAACAGCACTATCATCGGGTTT	662			
Db	601	ACCACTCCCTCGGAAACAGATACATGGCTCTTATCCAAACAGCACTATCATCGGGTTT	660			
Qy	663	TCTCAGGTGTTTGAAGCCACACAGAGAGAAACAAACCGGAGCTTCAGTGGTATCCAGTG	722			
Db	661	TCTCAGGTGTTTGAAGCCACACAGAGAGAAACAAACCGGAGCTTCAGTGGTATCCAGTG	720			
Qy	723	ACTGGGATGATGAAGGTCTAGCTGCTGAGCTGCTTATTTCTTCTTCTTCTTCTTCTTCT	782			
Db	721	ACTGGGATGATGAAGGTCTAGCTGCTGAGCTGCTTATTTCTTCTTCTTCTTCTTCTTCT	780			
Qy	783	GACTGCATCCGACATAAAGAAACAGTTGTCTCTGCCCAACAGCGCTCCCTTTCCCT	842			
Db	781	GACTGCATCCGACATAAAGAAACAGTTGTCTCTGCCCAACAGCGCTCCCTTTCCCT	840			
Qy	843	CTGGATTAACAAACAAAGCAAGCGGAGGCTGGCTGCCTCTCTCTCTCTCTCTCTCTCT	902			
Db	841	CTGGATTAACAAACAAAGCAAGCGGAGGCTGGCTGCCTCTCTCTCTCTCTCTCTCTCT	900			
Qy	903	GTGGCCACATGGTGTGTGTGGAGGATCTATCTAATGTGGAGGACAAAGGATCAAG	962			
Db	901	GTGGCCACATGGTGTGTGTGGAGGATCTATCTAATGTGGAGGACAAAGGATCAAG	960			
Qy	963	AAGACTTCTCTTTTCTACCAACCACTACTGCCCCCAATTAAGTTCTTGTGTTTACCCA	1022			
Db	961	AAGACTTCTCTTTTCTACCAACCACTACTGCCCCCAATTAAGTTCTTGTGTTTACCCA	1020			

Qy	1023	TCTGAAATATGTTTCCATCACAAATTTGTACTTCTCAGTGAATTTCTTCAAAACCAATTGC	1082
Db	1021	TCTGAAATATGTTTCCATCACAAATTTGTACTTCTCAGTGAATTTCTTCAAAACCAATTGC	1080
Qy	1083	AGAGTGAAGTGCATCTTCAAAAGTGGCAGAAAGAAATAGCAGATGGTCCAGTG	1142
Db	1081	AGAGTGAAGTGCATCTTCAAAAGTGGCAGAAAGAAATAGCAGATGGTCCAGTG	1140
Qy	1143	CAGTGGCTTGGCCACTCAAAAGAGGCGAGACAAAGTGGTCTTCTTCTTCTTCTTCAATGAC	1202
Db	1141	CAGTGGCTTGGCCACTCAAAAGAGGCGAGACAAAGTGGTCTTCTTCTTCTTCTTCAATGAC	1200
Qy	1203	GTCAACAGTGTGTGCGATGGTACCTGTGTGGAAGAGGCGAGTCCAGTGAAGTCTCT	1262
Db	1201	GTCAACAGTGTGTGCGATGGTACCTGTGTGGAAGAGGCGAGTCCAGTGAAGTCTCT	1260
Qy	1263	CAAGACTCTTCCCTTCCCTTAACTTTTCTGAGTGAATCAAGAGGCGAGATTCAT	1322
Db	1261	CAAGACTCTTCCCTTCCCTTAACTTTTCTGAGTGAATCAAGAGGCGAGATTCAT	1320
Qy	1323	CTGCACAAATACGTGGTGGTCTTCTTACAGAGATTTGATACAAAGACGATTACAAATGCT	1382
Db	1321	CTGCACAAATACGTGGTGGTCTTCTTACAGAGATTTGATACAAAGACGATTACAAATGCT	1380
Qy	1383	CTCAGTGTCTGCCCCCAAGTACCACTTCAATGAAGGATGCGCTTCTGTGCGAGAACTT	1442
Db	1381	CTCAGTGTCTGCCCCCAAGTACCACTTCAATGAAGGATGCGCTTCTGTGCGAGAACTT	1440
Qy	1443	CTCCATGTCAAGCAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1502
Db	1441	CTCCATGTCAAGCAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1500
Qy	1503	TGCTCTCTTGTAGCCCAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1562
Db	1501	TGCTCTCTTGTAGCCCAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1560
Qy	1563	TACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1622
Db	1561	TACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1620
Qy	1623	TAAATTAACATTTTATACCAATTAATTTTCAAAATTTTCAAAATTTTCAAAATTTTCA	1682
Db	1621	TAAATTAACATTTTATACCAATTAATTTTCAAAATTTTCAAAATTTTCAAAATTTTCA	1680
Qy	1683	TAAAGATTGGAATACATTTTCAAACTTCAAACTTCAAACTTCAAACTTCAAACTTCAAA	1742
Db	1681	TAAAGATTGGAATACATTTTCAAACTTCAAACTTCAAACTTCAAACTTCAAACTTCAAA	1740
Qy	1743	GCTTTAATGAAACTGTAACCAATTTTGAATGTAATGTAATGTAATGTAATGTAATGTAAT	1794
Db	1741	GCTTTAATGAAACTGTAACCAATTTTGAATGTAATGTAATGTAATGTAATGTAATGTAAT	1792

RESULT 4
 US-09-886-404-19
 ; Sequence 19, Application US/09886404
 ; Patent No. US20020037524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Medlock, Eugene
 ; APPLICANT: Yeh, Richard
 ; APPLICANT: Silbiger, Scott M.
 ; APPLICANT: Elliot, Gary S.
 ; APPLICANT: Nguyen, Hung Q.
 ; APPLICANT: Jing, Shugian
 ; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
 ; FILE REFERENCE: 01017/37128B
 ; CURRENT APPLICATION NUMBER: US/09/886.404
 ; CURRENT FILING DATE: 2001-06-21
 ; PRIOR APPLICATION NUMBER: 09/810,384
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/266,159
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 60/213,125

Db	885	AGGTGTTTGAGCCACACCAAGAAACAAACCGGAGCTTCACTGGTGATTCACGTGACTG	944
Qy	727	GGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCAATATTTTCTTACTATGTGGCAGCGACT	786
Db	945	GGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCAATATTTTCTTACTATGTGGCAGCGACT	1004
Qy	787	GCATCCGACATAAAGGAAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTTCCCTCTGG	846
Db	1005	GCATCCGACATAAAGGAAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTTCCCTCTGG	1064
Qy	847	ATAACACAAACGACGAGCGGAGGCTGCTGCCCTCTCTCTGCTGCTCTGCTGGTGG	906
Db	1065	ATAACACAAACGACGAGCGGAGGCTGCTGCCCTCTCTCTGCTGCTCTGCTGGTGG	1124
Qy	907	CCACATGGGTGCTGTGGCAGGGATCTATCTAATGTGGAGGCAAGAAAGATCAAGAAGA	966
Db	1125	CCACATGGGTGCTGTGGCAGGGATCTATCTAATGTGGAGGCAAGAAAGATCAAGAAGA	1184
Qy	967	CTTCTCTTTCTACCAACAACACTACTGCCCCCAATTAAGGTTCTGTGTGTTTACCCTCTG	1026
Db	1185	CTTCTCTTTCTACCAACAACACTACTGCCCCCAATTAAGGTTCTGTGTGTTTACCCTCTG	1244
Qy	1027	AAATATGTTTCCATCACAAATTTGTTACTTCACTGAATTTCTTCAAACCAATTCGAGAA	1086
Db	1245	AAATATGTTTCCATCACAAATTTGTTACTTCACTGAATTTCTTCAAACCAATTCGAGAA	1304
Qy	1087	GTGAGGTCACTCTTGAAGAGTGGCAGAAAGAAATAGCAGAGATGGGTCCAGTGCAGT	1146
Db	1305	GTGAGGTCACTCTCGAAGAGTGGCAGAAAGAAATAGCAGAGATGGGTCCAGTGCAGT	1364
Qy	1147	GGCTTGGCACTCAAAAGAGGACAGACAAAGTCGTCTTCTTCTTCCAAATGACGTCA	1206
Db	1365	GGCTTGGCACTCAAAAGAGGACAGACAAAGTCGTCTTCTTCTTCCAAATGACGTCA	1424
Qy	1207	ACAGTGTGCGAGTGTACTGTGGCAAGCGAGGGCAGTCCACGTGAGAACTCTCAAG	1266
Db	1425	ACAGTGTGCGAGTGTACTGTGGCAAGCGAGGGCAGTCCACGTGAGAACTCTCAAG	1484
Qy	1267	ACCTCTTCCCTTGCCTTTTAACTTTCTGCAGTGTACTAAGAGCCAGATTCATCTGC	1326
Db	1485	ACCTCTTCCCTTGCCTTTTAACTTTCTGCAGTGTACTAAGAGCCAGATTCATCTGC	1544
Qy	1327	ACAAATACGTGTGGTCTACTTTTAGAGAGATTGATACAAAGACGATTCACATCTCA	1386
Db	1545	ACAAATACGTGTGGTCTACTTTTAGAGAGATTGATACAAAGACGATTCACATCTCA	1604
Qy	1387	GTGCTGTGCCCCAAGTACCACTTCATGAGGATGCCACTGCTTTCTGTGTCGAGAACTTCC	1446
Db	1605	GTGCTGTGCCCCAAGTACCACTTCATGAGGATGCCACTGCTTTCTGTGTCGAGAACTTCC	1664
Qy	1447	ATGTCAAGCAGCAGGTGTACAGGAGAAAGATCAAGCCCTGCCACGATGGCTGCTGCT	1506
Db	1665	ATGTCAAGCAGCAGGTGTACAGGAGAAAGATCAAGCCCTGCCACGATGGCTGCTGCT	1724
Qy	1507	CCTTGTAGCCCAACCCATGAGAAAGACGCTTAAAGGCTTCTATCCCAACCAATTACA	1566
Db	1725	CCTTGTAGCCCAACCCATGAGAAAGACGCTTAAAGGCTTCTATCCCAACCAATTACA	1784
Qy	1567	GGGAAAAACGCTGTGATGATCTCTGAAGCTTACTATGCAGCCCTACAAACAGCCTTAGTAAT	1626
Db	1785	GGGAAAAACGCTGTGATGATCTCTGAAGCTTACTATGCAGCCCTACAAACAGCCTTAGTAAT	1844
Qy	1627	TAAAAACATTTTATACCAATAAAATTTTCAATATTTACTTAACCTTAATGTAGCAATTAAC	1686
Db	1845	TAAAAACATTTTATACCAATAAAATTTTCAATATTTACTTAATGTAGCAATTAAC	1904
Qy	1687	GATTGGAAACTACATTTTACAACTTCAAGCTGTGTTTTATACATAGAAATCAATTAACGCTT	1746
Db	1905	GATTGGAAACTACATTTTACAACTTCAAGCTGTGTTTTATACATAGAAATCAATTAACGCTT	1964
Qy	1747	TAATTGAAAACGTGAACCATTTTGTGATTAATGCAACCAATTAAGCATCTTC	1794

Db 542 TGTGGATCGAATCATCTGTTGTAAGAGATAGGAGACAGTAGAAGTAATCTCA 601
Qy 601 CAACCACTCCCTGGGAAACAGATACATGGCTCTTATCAACACAGCACTATCATCGGCT 660
Db 602 CAACCACTCCCTGGGAAACAGATACATGGCTCTTATCAACACAGCACTATCATCGGCT 661
Qy 661 TTCTCAGGTGTTGAGCCACACACCAAGAAACAAACGCGGCTTCAGTGTGATCCAG 720
Db 662 TTCTCAGGTGTTGAGCCACACACCAAGAAACAAACGCGGCTTCAGTGTGATCCAG 721
Qy 721 TCACTGGGATAGTGAAGTGTCTACGGTGCAGCTGACTCCATATTTCTACTTTGGGCA 780
Db 722 TCACTGGGATAGTGAAGTGTCTACGGTGCAGCTGACTCCATATTTCTACTTTGGGCA 781
Qy 781 GGAATGATCCGACATAAAGAAACAGTTGTCTCTGCCCAACAAACAGCGCTCCCTTTCC 840
Db 782 GCGACTGTCATCCGACATAAAGAAACAGTTGTCTCTGCCCAACAAACAGCGCTCCCTTTCC 841
Qy 841 CTCTGGATTAACAAACAAACGCGGAGGTGGCTGCTCTCTCTCTCTCTCTCTCTCTGC 900
Db 842 CTCTGGATTAACAAACAAACGCGGAGGTGGCTGCTCTCTCTCTCTCTCTCTCTCTGC 901
Qy 901 TGTGGCCACATGGGTGCTGGTGGACAGGATCTATCTAATGTGGAGGACAGAAAGGATCA 960
Db 902 TGTGGCCACATGGGTGCTGGTGGACAGGATCTATCTAATGTGGAGGACAGAAAGGATCA 961
Qy 961 AGAAGACTCTCTTTTACCAACACACTACTGCCCCCACTTAAGGTTCTTGTGGTTTACC 1020
Db 962 AGAAGACTCTCTTTTACCAACACACTACTGCCCCCACTTAAGGTTCTTGTGGTTTACC 1021
Qy 1021 CATCTGAATATGTTTCCATACACAAATTTGTAATCTCACTGAATTTCTTCAAAACAT 1080
Db 1022 CATCTGAATATGTTTCCATACACAAATTTGTAATCTCACTGAATTTCTTCAAAACAT 1081
Qy 1081 GCAGAGTCAGGTCTCTTTGAAAGTGCAGAAAGAAATAGCAGAGATGGTGGTCCAG 1140
Db 1082 GCAGAGTCAGGTCTCTTTGAAAGTGCAGAAAGAAATAGCAGAGATGGTGGTCCAG 1141
Qy 1141 TGCAGTGGCTTGCCTCAAAAGAGGACAGACAAAGTCTCTTCTTTTCAATG 1200
Db 1142 TGCAGTGGCTTGCCTCAAAAGAGGACAGACAAAGTCTCTTCTTTTCAATG 1201
Qy 1201 AGTCACAGTGTGCGATGTTACTGTGGCAAGAGGAGGAGTCCAGTGAAGT 1260
Db 1202 AGTCACAGTGTGCGATGTTACTGTGGCAAGAGGAGGAGTCCAGTGAAGT 1261
Qy 1261 CTCAGACCTCTTCCCTTGCCTTTAACTTTCTGCAAGTATCTAAGAGCCAGATTC 1320
Db 1262 CTCAGACCTCTTCCCTTGCCTTTAACTTTCTGCAAGTATCTAAGAGCCAGATTC 1321
Qy 1321 ATCTGCAAAATACGTGGTGGTCTACTTTAGAGAGTTGATACAAAGACGATTACAATG 1380
Db 1322 ATCTGCAAAATACGTGGTGGTCTACTTTAGAGAGTTGATACAAAGACGATTACAATG 1381
Qy 1381 CTCTCAGTGTGCCCCCAAGTACCACTCATGAAGATGCCACTGTTCTGTGCAAGAC 1440
Db 1382 CTCTCAGTGTGCCCCCAAGTACCACTCATGAAGATGCCACTGTTCTGTGCAAGAC 1441
Qy 1441 TTCTCCATCTCAGCAGAGGTGTACAGAGGAAAGATCAAGGCTCCACGATGGCT 1500
Db 1442 TTCTCCATCTCAGCAGAGGTGTACAGAGGAAAGATCAAGGCTCCACGATGGCT 1501
Qy 1501 GCTGCTCTCTTGTAG 1514
Db 1502 GCTGCTCTCTTGTAG 1515

RESULT 6

US-10-000-157-11

; Sequence 11, Application US/10000157

; Publication No. US20020182673A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul L.
; APPLICANT: Grimaldi, J.Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovasnik, Melissa.
; APPLICANT: VanLookeren, Menno
; APPLICANT: Watanabe, Richard
; APPLICANT: Williams, P.Wickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1CIP4 (US)
; CURRENT APPLICATION NUMBER: US/10/000,157
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/172096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/175481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/213807
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/242837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/244072
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/253646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/908827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/931836

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, PRIOR FILING DATE: 2001-08-16
, PRIOR APPLICATION NUMBER: PCT/US99/05028
, PRIOR FILING DATE: 1999-03-08
, PRIOR APPLICATION NUMBER: PCT/US99/10733
, PRIOR FILING DATE: 1999-05-14
, PRIOR APPLICATION NUMBER: PCT/US99/31274
, PRIOR FILING DATE: 1999-12-30
, PRIOR APPLICATION NUMBER: PCT/US00/04341
, PRIOR FILING DATE: 2000-02-18
, PRIOR APPLICATION NUMBER: PCT/US00/05601
, PRIOR FILING DATE: 2001-03-01
, PRIOR APPLICATION NUMBER: PCT/US00/05841
, PRIOR FILING DATE: 2000-03-02
, PRIOR APPLICATION NUMBER: PCT/US00/07532
, PRIOR FILING DATE: 2000-03-21
, PRIOR APPLICATION NUMBER: PCT/US00/15264
, PRIOR FILING DATE: 2000-06-02
, PRIOR APPLICATION NUMBER: PCT/US00/23328
, PRIOR FILING DATE: 2000-08-24
, PRIOR APPLICATION NUMBER: PCT/US00/30873
, PRIOR FILING DATE: 2000-11-10
, PRIOR APPLICATION NUMBER: PCT/US00/32678
, PRIOR FILING DATE: 2000-12-01
, PRIOR APPLICATION NUMBER: PCT/US00/34956
, PRIOR FILING DATE: 2000-12-20
, PRIOR APPLICATION NUMBER: PCT/US01/00520
, PRIOR FILING DATE: 2001-02-28
, PRIOR APPLICATION NUMBER: PCT/US01/17800
, PRIOR FILING DATE: 2001-06-01
, PRIOR APPLICATION NUMBER: PCT/US01/19692
, PRIOR FILING DATE: 2001-06-20
, PRIOR APPLICATION NUMBER: PCT/US01/21066
, PRIOR FILING DATE: 2001-06-29
, PRIOR APPLICATION NUMBER: PCT/US01/21735
, PRIOR FILING DATE: 2001-07-09
, NUMBER OF SEQ ID NOS: 39
, SEQ ID NO 11
, LENGTH: 1515
, TYPE: DNA
, ORGANISM: Homo Sapien
US-10-000-157-11

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Query Match	82.6%	Score 1509.2	DB 9	Length 1515
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1511	Conservative 0	Mismatches 3	Indels 0	Gaps 0
Qy	1	CGGCGATGTCGTCTGCTGTGATAAGCCTGGCCGCGCTGTGCAGGAGCGCGTACCCCGAG	60	
Db	2	CGGCGATGTCGTCTGCTGTGATAGCCTGGCCGCGCTGTGCAGGAGCGCGTACCCCGAG	61	
Qy	61	AGCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATG	120	
Db	62	AGCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATG	121	
Qy	121	ATCTAATCCCCGGAGACTTGGGGACCTCCGAGTAGAACCTGTTCACACTAGTGTTCGAA	180	
Db	122	ATCTAATCCCCGGAGACTTGGGGACCTCCGAGTAGAACCTGTTCACACTAGTGTTCGAA	181	
Qy	181	CAGGGGACTATTCAAATTTTGATGATTAAGCTGGGTACTCCGGGCAGATGCCAGCATCC	240	
Db	182	CAGGGGACTATTCAAATTTTGATGATTAAGCTGGGTACTCCGGGCAGATGCCAGCATCC	241	
Qy	241	GCTTGTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAATTCAGTCTCTACAGCT	300	
Db	242	GCTTGTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAATTCAGTCTCTACAGCT	301	
Qy	301	GTGTGAGGTGCAATTTACACAGAGGCTTCCAGACTTCAGACGAGCCCTCTGGTGGTAAAT	360	
Db	302	GTGTGAGGTGCAATTTACACAGAGGCTTCCAGACTTCAGACGAGCCCTCTGGTGGTAAAT	361	
Qy	361	GGACATTTTCCTATATCGGCTTCCCTGTGTAGAGCTGAACACAGTCTATTTCATTTGGGGCCC	420	
Db	362	GGACATTTTCCTATATCGGCTTCCCTGTGTAGAGCTGAACACAGTCTATTTCATTTGGGGCCC	421	

Db 1202 ACCTCAACAGTGTGTCGGTGTACCTGTGGCAAGAGCGAGGCGAGTCCAGTGAGAACT 1261
Qy 1261 CTCAGAGACTCTTCCCTTGCCTTTAACTTTCTGCAAGTATCTAAGAGCCAGATTC 1320
Db 1262 CTCAGAGACTCTTCCCTTGCCTTTAACTTTCTGCAAGTATCTAAGAGCCAGATTC 1321
Qy 1321 ATCTGCAAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAGAGGATTACAATG 1380
Db 1322 ATCTGCAAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAGAGGATTACAATG 1381
Qy 1381 CTCTCAGTGTCTGCCCCCAAGTACCCTCATGAAGATGCCCTGCTTCTGTGCAAGAAC 1440
Db 1382 CTCTCAGTGTCTGCCCCCAAGTACCCTCATGAAGATGCCCTGCTTCTGTGCAAGAAC 1441
Qy 1441 TTCTCCATGTCAGCAGCAGGTGTGTCAGCAGGAGAAAGATCACAGCCTGCCAGATGGCT 1500
Db 1442 TTCTCCATGTCAGCAGCAGGTGTGTCAGCAGGAGAAAGATCACAGCCTGCCAGATGGCT 1501
Qy 1501 GCTGCTCCTGTAG 1514
Db 1502 GCTGCTCCTGTAG 1515

RESULT 9
US-10-174-590-399
; Sequence 399, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RLC42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-399

Query Match 82.6%; Score 1509.2; DB 9; Length 1515;
Best Local Similarity 99.8%; Pred. No. 0; Mismatches 0; Gaps 0;
Matches 1511; Conservative 0; Indels 3; Indels 0; Gaps 0;

Qy 1 CGCGGATGTCGTCTGTGATGAAGCTCGCGCGCTGTGCGAGGCGCGCTACCCCGAG 60
Db 2 CGCGGATGTCGTCTGTGATGAAGCTCGCGCGCTGTGCGAGGCGCGCTACCCCGAG 61
Qy 61 AGCCGACGTTCAATGTGGCTCTGAAATCGGGCCATCTCCAGATGGATGCTACAAATG 120
Db 62 AGCCGACGTTCAATGTGGCTCTGAAATCGGGCCATCTCCAGATGGATGCTACAAATG 121
Qy 121 ATCTAATCCCGGACCTTGGGACCTCCGAGTAGAAGCTCTTCACTAGTGTGCA 180
Db 122 ATCTAATCCCGGACCTTGGGACCTCCGAGTAGAAGCTCTTCACTAGTGTGCA 181
Qy 181 CAGGGGACTATTCAATTTTGTATGTAAAGCTGGGTACTCCGGGCGAGATGCCAGATCC 240
Db 182 CAGGGGACTATTCAATTTTGTATGTAAAGCTGGGTACTCCGGGCGAGATGCCAGATCC 241
Qy 241 GCTTGTGAAGCCCAAGATTTGTGTGA CGGGCAAGCAACTTCCAGTCTCTACAGT 300

Db 242 GCTTGTGAAGCCCAAGATTTGTGTGACGGGCAAGCAACTTCCAGTCTCTACAGT 301
Qy 301 GTGTGAGGTGCAATTTACACAGAGGCTTCCAGACTCAGACAGACCTCTGTGGTAAAT 360
Db 302 GTGTGAGGTGCAATTTACACAGAGGCTTCCAGACTCAGACAGACCTCTGTGGTAAAT 361
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Db 362 GGAATTTTCTTATATGCGCTTCCCTGTAGAGCTGAAACAAGTCTATTTTCAATTTGGGGCC 421
Qy 421 ATAATATTCTTAATGCAATATGAATGAAGTGGCCCTTCCATGTCTGTGAATTTCACT 480
Db 422 ATAATATTCTTAATGCAATATGAATGAAGTGGCCCTTCCATGTCTGTGAATTTCACT 481
Qy 481 CACAGGCTGCTAGACACACATAATGAAATATAAAAAAAGTGTGCAAGGCGCGAAGCC 540
Db 482 CACAGGCTGCTAGACACACATAATGAAATATAAAAAAAGTGTGCAAGGCGCGAAGCC 541
Qy 541 TGTGGATCCGAAATCACTGCTTGTAAAGAAATGAGGAGACAGTAGAAGTGAATTTCA 600
Db 542 TGTGGATCCGAAATCACTGCTTGTAAAGAAATGAGGAGACAGTAGAAGTGAATTTCA 601
Qy 601 CAACCACTCCCTGGGAAACAGATACATGGCTTTATCCAAACACAGCACTATCATCGGT 660
Db 602 CAACCACTCCCTGGGAAACAGATACATGGCTTTATCCAAACACAGCACTATCATCGGT 661
Qy 661 TTTCTCAGGTGTTGAGCCACACAGAGAAACAAACGAGCTTTCAGTGGTGAATTTCCAG 720
Db 662 TTTCTCAGGTGTTGAGCCACACAGAGAAACAAACGAGCTTTCAGTGGTGAATTTCCAG 721
Qy 721 TGACTGGGATAGTCAAGGTGCTACGGTGCAGCTCACTCCATATTTTCTACTTTGGCA 780
Db 722 TGACTGGGATAGTCAAGGTGCTACGGTGCAGCTCACTCCATATTTTCTACTTTGGCA 781
Qy 781 GCGACTGCATCCGACATAAAGAACAGTTGTCTGCTGCCCAACACAGCGCTCCCTTTCC 840
Db 782 GCGACTGCATCCGACATAAAGAACAGTTGTCTGCTGCCCAACACAGCGCTCCCTTTCC 841
Qy 841 CTCTGGATAACAAACAAAGAGCGGAGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 842 CTCTGGATAACAAACAAAGAGCGGAGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCT 901
Qy 901 TGGTGGCCACATGGTGTGCTGGGAGGATCTCTAATGTGAGGACGCAAGAGATCA 960
Db 902 TGGTGGCCACATGGTGTGCTGGGAGGATCTCTAATGTGAGGACGCAAGAGATCA 961
Qy 961 AGAAGACTTCTTTTCTACCCACACACTACTGCCCCCACTTAAGGTTCCTTGTGGTTTACC 1020
Db 962 AGAAGACTTCTTTTCTACCCACACACTACTGCCCCCACTTAAGGTTCCTTGTGGTTTACC 1021
Qy 1021 CATCTGAAATATGTTTCCATCACACAAATTTGTACTTCACTGAATTTCTTCAAAACCAT 1080
Db 1022 CATCTGAAATATGTTTCCATCACACAAATTTGTACTTCACTGAATTTCTTCAAAACCAT 1081
Qy 1081 GCAGAAGTGAGTCACTCTTGAAGAGTGGCAGAAAGAAATAGCAGAGATGGGTCCAG 1140
Db 1082 GCAGAAGTGAGTCACTCTTGAAGAGTGGCAGAAAGAAATAGCAGAGATGGGTCCAG 1141
Qy 1141 TGCAAGTGGCTGCACTCAAAAGAGGAGCAGACAAAGTGTCTCTTCTTTTCAATG 1200
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Db 1202 AGCTCAACAGTGTGCGATGCTGCTGCAAGAGGAGGAGCTCCAGTAGAGACT 1261
Qy 1261 CTCAGAAGCTCTTCCCTTGAACCTTTTCTGAGTGAATCTAAGAGAGCCAGATTC 1320
Db 1262 CTCAGAAGCTCTTCCCTTGAACCTTTTCTGAGTGAATCTAAGAGAGCCAGATTC 1321
Qy 1321 ATCTGCAAAATACGTGGTGTCTACTTTAGAGATTTGATACAAAGACGATTTCAATG 1380

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Db 1322 ATCTGCACAAATACGTGGTGTCTACTTTAGAGAGATTGATACAAAGACGATTACAATG 1381
Qy 1381 CTCTCAGTGTCTGCCCCAAGTAGTACCACTTCATGAAGGATGCCACTGTTTCTGTGCAGAAC 1440
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Qy 1441 TTCTCCATGTCGAAGCAGCAGGTGTGAGCAGGAGAAAGATCAACAGCCTGCCACGATGGCT 1500
Db 1442 TTCTCCATGTCGAAGCAGCAGGTGTGAGCAGGAGAAAGATCAACAGCCTGCCACGATGGCT 1501
Qy 1501 GCTGCTCTCTGTAG 1514
Db 1502 GCTGCTCTCTGTAG 1515

RESULT 10
US-10-176-758-399
; Sequence 399, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-758-399

Query Match 82.6%; Score 1509.2; DB 9; Length 1515;
Best Local Similarity 99.8%; Pred. No. 0; Mismatches 3; Indels 0; Gaps 0;
Matches 1511; Conservative 0;

Qy 1 CGGCGATGTCGTCTGCTGATAGCCTGGCCGCGCTGTGCAGGAGCGCGTACCCCGAG 60
Db 2 CGGCGATGTCGTCTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCGTACCCCGAG 61
Qy 61 AGCCGACCGTTCAATGTGCTCTGAACCTGGGCGCATCTCCAGAGTGGATGCTACAACATG 120
Db 62 AGCCGACCGTTCAATGTGCTCTGAACCTGGGCGCATCTCCAGAGTGGATGCTACAACATG 121
Qy 121 ATCTTAATCCCGAGACTTGGAGGACCTCCGAGTAGAACCTGTACAACTAGTGTGCAA 180
Db 122 ATCTTAATCCCGAGACTTGGAGGACCTCCGAGTAGAACCTGTACAACTAGTGTGCAA 181
Qy 181 CAGGGGACTATTCAATTTTGTGAATGTAAAGCTGGGTACTCCGGGCGAGATGCCAGATCC 240
Db 182 CAGGGGACTATTCAATTTTGTGAATGTAAAGCTGGGTACTCCGGGCGAGATGCCAGATCC 241
Qy 241 GCTTCTGAGGCGCCACAGATTGTGTGACCGGCAAGCAACTCCAGTCTTACAGCT 300
Db 242 GCTTGTGAAGCGCCACAGATTGTGTGACCGGCAAGCAACTTCCAGTCTTACAGCT 301
Qy 301 GTGTGAGGTGCAATTACACAGAGGCGCTTCCAGACTCAGACACAGACCTCTGGTGGTAAAT 360
Db 302 GTGTGAGGTGCAATTACACAGAGGCGCTTCCAGACTCAGACACAGACCTCTGGTGGTAAAT 361
Qy 361 GGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACACAGCTCTATTTCATTGGGGGCC 420
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Db 362 GGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACACAGCTCTATTTCATTGGGGGCC 421
Qy 421 ATAATATTTCTTAATGCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACT 480
Db 422 ATAATATTTCTTAATGCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACT 481
Qy 481 CACCAGGCTGCTAGACACACATAATGAAATATAAAAAAAGTGTCAAGCGCGGAAGCC 540
Db 482 CACCAGGCTGCTAGACACACATAATGAAATATAAAAAAAGTGTCAAGCGCGGAAGCC 541
Qy 541 TGTGGGATCCGAACATCACTGTTGTGAAGAATAGAGGACAGTAGAAGTGAACCTTCA 600
Db 542 TGTGGGATCCGAACATCACTGTTGTGAAGAATAGAGGACAGTAGAAGTGAACCTTCA 601
Qy 601 CAACCACTCCCTCGGAAACAGATACATGGCTTTATCCAAACACAGCACTATCATCGGCT 660
Db 602 CAACCACTCCCTCGGAAACAGATACATGGCTTTATCCAAACACAGCACTATCATCGGCT 661
Qy 661 TTTCTCAGGTGTTTGAGCCACACAGAAAGAAACAAACCGAGCTTTCAGTGGTGAATCCAG 720
Db 662 TTTCTCAGGTGTTTGAGCCACACAGAAAGAAACAAACCGAGCTTTCAGTGGTGAATCCAG 721
Qy 721 TGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACATCCATATTTTCTCTTCTGTGGCA 780
Db 722 TGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACATCCATATTTTCTCTTCTGTGGCA 781
Qy 781 GCGACTGCATCCGACATAAAGGAACAGTGTCTCTGCCCAACAAACAGCGCTTCCCTTCC 840
Db 782 GCGACTGCATCCGACATAAAGGAACAGTGTCTCTGCCCAACAAACAGCGCTTCCCTTCC 841
Qy 841 CTCTGGATAACAAACAAAGCAGCGGAGCTGGCTGCCTCTCTCTCTCTCTCTCTCTCTCTGC 900
Db 842 CTCTGGATAACAAACAAAGCAGCGGAGCTGGCTGCCTCTCTCTCTCTCTCTCTCTCTCTGC 901
Qy 901 TGTGGGCCACATGGGTGCTGTGGCAGGGATCTATCTAATGTGGAGGACCAAGAGGATCA 960
Db 902 TGTGGGCCACATGGGTGCTGTGGCAGGGATCTATCTAATGTGGAGGACCAAGAGGATCA 961
Qy 961 AGAAGACTTCTCTTTCTACCACCACTACTGCCCCCATTAAGGTCTCTGTGGTTTACC 1020
Db 962 AGAAGACTTCTCTTTCTACCACCACTACTGCCCCCATTAAGGTCTCTGTGGTTTACC 1021
Qy 1021 CATCTGAAATATGTTTCCATCACACAAATTTGTACTTCACTGAATTTCTTCAAAACCAATT 1080
Db 1022 CATCTGAAATATGTTTCCATCACACAAATTTGTACTTCACTGAATTTCTTCAAAACCAATT 1081
Qy 1081 GCAGAAGTGAGGTCACTCTTGAAAGTGGCAGAAAGAAATAGCAGAGATGGGTCCAG 1140
Db 1082 GCAGAAGTGAGGTCACTCTTGAAAGTGGCAGAAAGAAATAGCAGAGATGGGTCCAG 1141
Qy 1141 TGCAGTGGCTTGGCACTCAAAAGAGGACGACAGCAAAAGTCTCTCTCTTCTTCCAATG 1200
Db 1142 TGCAGTGGCTTGGCACTCAAAAGAGGACGACAGCAAAAGTCTCTCTCTTCTTCCAATG 1201
Qy 1201 ACGTCAACAGTGTGTGGTACCTGTGTGCAAGAGGAGGAGGAGTCCAGTGAAGAACT 1260
Db 1202 ACGTCAACAGTGTGTGGTACCTGTGTGCAAGAGGAGGAGGAGTCCAGTGAAGAACT 1261
Qy 1261 CTCAAGACTCTTCTCCCTTTCCTTTTAACTTTTCTGAGTGTATTAAGAGCCAGATTC 1320
Db 1262 CTCAAGACTCTTCTCCCTTTCCTTTTAACTTTTCTGAGTGTATTAAGAGCCAGATTC 1321
Qy 1321 ATCTGCACAAATAGTGGTGTCTACTTTTAGAGAGATTGATACAAAAGACGATTACAATG 1380
Db 1322 ATCTGCACAAATAGTGGTGTCTACTTTTAGAGAGATTGATACAAAAGACGATTACAATG 1381
Qy 1381 CTCTCAGTGTCTGCCCCAAGTACCACTTTCATGAAGGATGCCACTGCTTCTGTGCAGAAC 1440
Db 1382 CTCTCAGTGTCTGCCCCAAGTACCACTTTCATGAAGGATGCCACTGCTTCTGTGCAGAAC 1441
Qy 1441 TTCTCCATGTCGAAGCAGGTGTGAGCAGGAGAAAGATCAACAGCCTGCCACGATGGCT 1500
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Db 1442 TTCTCCATGTCAGACGACGGTGTGACGAGGAAAAAAGATCAACAAGCCTGCCACGATGGCT 1501
Qy 1501 GCTGCTCCTTTGTAG 1514
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      |||||
Db 1502 GCTGCTCCTTTGTAG 1515

RESULT 11
US-10-063-616-157
; Sequence 157, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 157
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-157

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RESULT 12
US-10-175-737-399
; Sequence 399, Application US/10175737

D	b	782	GCGACTGCATCCGACATAAAGGAACAAGTTGTGCTCTGCCCAAAAACAGGCGTCCCTTTCCC	841
Q	y	841	CTCTGGATAAACAAACAAAGCAAGC CGGAGGTCGCTCTCCTCCTGCTGTCTCTGC	900
D	b	842	CTCTGGATAAACAAACAAAGCAAGC CGGAGGTCGCTCTCCTCCTGCTGTCTCTGC	901
Q	y	901	TGTTGGCCACATGGTGCTGGTGGCAGGGATCTATCTAAATGTGGAGGCACGAAAGGATCA	960
D	b	902	TGTTGGCCACATGGTGCTGGTGGCAGGGATCTATCTAAATGTGGAGGCACGAAAGGATCA	961
Q	y	961	AGAAGACTTCCTTTTTCACACACACTACTGCCCCCATTAAAGTTCTTTGTGGTTTTACC	1020
D	b	962	AGAAGACTTCCTTTTTCACACACACTACTGCCCCCATTAAAGTTCTTTGTGGTTTTACC	1021
Q	y	1021	CATCTGAAAAATATGTTTCCATCACACAATTTGTTACTCTGAATTTCTTCAAACCATT	1080
D	b	1022	CATCTGAAAAATATGTTTCCATCACACAATTTGTTACTCTGAATTTCTTCAAACCATT	1081
Q	y	1081	GCAGAAGTAGGTCATCCTTTGAAAAAGTGGCAGAAAAAGAAAAATAGCAGAGATGGGTCCAG	1140
D	b	1082	GCAGAAGTAGGTCATCCTTTGAAAAAGTGGCAGAAAAAGAAAAATAGCAGAGATGGGTCCAG	1141
Q	y	1141	TGCAGTGGCTTGCCACTCAAAGAAAGGCAGCAGACAAAGTCGTCTCTCTTTCCAATG	1200
D	b	1142	TGCAGTGGCTTGCCACTCAAAGAAAGGCAGCAGACAAAGTCGTCTCTCTTTCCAATG	1201
Q	y	1201	ACGTCAACAGTGTGCGATGGTACCTGTGGCAAGCGCAGGSGCAGTCCCACTGAGAACT	1260
D	b	1202	ACGTCAACAGTGTGCGATGGTACCTGTGGCAAGCGCAGGSGCAGTCCCACTGAGAACT	1261
Q	y	1261	CTCAAGACCTCTTCCCCTTGGCTTTTAACCTTTTCTGCAGTGATCTTAAGAGCCAGATTC	1320
D	b	1262	CTCAAGACCTCTTCCCCTTGGCTTTTAACCTTTTCTGCAGTGATCTTAAGAGCCAGATTC	1321
Q	y	1321	ATCTGCACAAATACGTGGTGCTCATCTTTAGAGAGATTGATACAAAGACGATTACAATG	1380
D	b	1322	ATCTGCACAAATACGTGGTGCTCATCTTTAGAGAGATTGATACAAAGACGATTACAATG	1381
Q	y	1381	CTCTCAGTGTCGCCCAAGTACCACTTCATGAAGATGCCACTGCTTCTGTGCGAGAAC	1440
D	b	1382	CTCTCAGTGTCGCCCAAGTACCACTTCATGAAGATGCCACTGCTTCTGTGCGAGAAC	1441
Q	y	1441	TTCTCCATGTCAAGACGACGGTGTCAGCAGGAAAAAGATCAAGCCTGCCACGATGGCT	1500
D	b	1442	TTCTCCATGTCAAGACGACGGTGTCAGCAGGAAAAAGATCAAGCCTGCCACGATGGCT	1501
Q	y	1501	GCTGCTCCTTG TAG 1514	
D	b	1502	GCTGCTCCTTG TAG 1515	
RESULT 14				
US-10-173-706-399				
; Sequence 399, Application US/10173706				
; Publication No. US2003002293A1				
; GENERAL INFORMATION:				
; APPLICANT: Baker, Kevin P.				
; APPLICANT: Chen, Jian				
; APPLICANT: Desnoyers, Luc				
; APPLICANT: Goddard, Audrey				
; APPLICANT: Godowski, Paul J.				
; APPLICANT: Gurney, Austin L.				
; APPLICANT: Pan, James				
; APPLICANT: Smith, Victoria				
; APPLICANT: Watanabe, Colin K.				
; APPLICANT: Wood, William I.				
; APPLICANT: Zhang, Zemin				
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC				
; FILE REFERENCE: P3430R1C7				
; CURRENT APPLICATION NUMBER: US/10/173,706				
; CURRENT FILING DATE: 2002-06-17				

; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 399
 ; LENGTH: 1515
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-173-706-399

Query Match 82.6%; Score 1509.2; DB 9; Length 1515;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1511; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	CGGCGATGCGTGTGCTGATGAAGCTGGCGCGCTGTGAGAGCGCGCTACCCCGAG	60
Db	2	CGGCGATGCGTGTGCTGATGAAGCTGGCGCGCTGTGAGAGCGCGCTACCCCGAG	61
Qy	61	AGCGGACCTTCAATGTGCTCTGAAGCTGGGCGCATCTCCAGAGTGGATCTACACATG	120
Db	62	AGCGGACCTTCAATGTGCTCTGAAGCTGGGCGCATCTCCAGAGTGGATCTACACATG	121
Qy	121	ATCTAATCCCGGAGACTTGGAGGACCTCCGAGTAGAAGCTGTACAACTAGTGTGCA	180
Db	122	ATCTAATCCCGGAGACTTGGAGGACCTCCGAGTAGAAGCTGTACAACTAGTGTGCA	181
Qy	181	CAGGGACTATTCAATTTTGTGATGAATGTAAAGCTGGGTACTCCGGGCGAGATGCCAGCATCC	240
Db	182	CAGGGACTATTCAATTTTGTGATGAATGTAAAGCTGGGTACTCCGGGCGAGATGCCAGCATCC	241
Qy	241	GCTTGTGAAGGCCACCAAGATTTGTGACGGGCAAAAGCACTTCCAGTCTTACAGCT	300
Db	242	GCTTGTGAAGGCCACCAAGATTTGTGACGGGCAAAAGCACTTCCAGTCTTACAGCT	301
Qy	301	GTGTGAGGTGCAATTAACAGAGGCTTCCAGACTCAGACAGACGCTCTGTGGTAAAT	360
Db	302	GTGTGAGGTGCAATTAACAGAGGCTTCCAGACTCAGACAGACGCTCTGTGGTAAAT	361
Qy	361	GGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACAGCTATTTTCATTTGGGGGCC	420
Db	362	GGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACAGCTATTTTCATTTGGGGGCC	421
Qy	421	ATAATATTTCTAATGAATATGAATGAAGTGGGCTTCCAGTCTGTGAATTTCACT	480
Db	422	ATAATATTTCTAATGAATATGAATGAAGTGGGCTTCCAGTCTGTGAATTTCACT	481
Qy	481	CACCGGCTGCTTAGACCAATTAATGAATATAAATAAAGTGTCAAGGCGGGAAGCC	540
Db	482	CACCGGCTGCTTAGACCAATTAATGAATATAAATAAAGTGTCAAGGCGGGAAGCC	541
Qy	541	TGTGGATCCGAACATCACTGTGTTGAAGAAATGAGAGACAGTGAAGTGAATTTCA	600
Db	542	TGTGGATCCGAACATCACTGTGTTGAAGAAATGAGAGACAGTGAAGTGAATTTCA	601
Qy	601	CAACCACTCCCTGGGAAACAGATATGCTTCTATCAACACAGCACTATCGGGT	660
Db	602	CAACCACTCCCTGGGAAACAGATATGCTTCTATCAACACAGCACTATCGGGT	661
Qy	661	TTTCTCAGGTGTTTGAAGCACACCAAGAAACAAACGCGAGCTTCAGTGGTGAATTC	720
Db	662	TTTCTCAGGTGTTTGAAGCACACCAAGAAACAAACGCGAGCTTCAGTGGTGAATTC	721
Qy	721	TGACTGGGATAGTGAAGTGTCTACGGTGCAGTGCATCTCATATTTTCTACTTTGGCA	780
Db	722	TGACTGGGATAGTGAAGTGTCTACGGTGCAGTGCATCTCATATTTTCTACTTTGGCA	781
Qy	781	GGACTGCAATCCGACATAAAGAAAGTGTGCTGTGCCCAAAACAGCGCTCCCTTCC	840
Db	782	GGACTGCAATCCGACATAAAGAAAGTGTGCTGTGCCCAAAACAGCGCTCCCTTCC	841
Qy	841	CTCTGGATAACCAACAAAGCAAGCGGAGGTGGTGGCTCTCTCTCTGTCTCTGC	900
Db	842	CTCTGGATAACCAACAAAGCAAGCGGAGGTGGTGGCTCTCTCTCTGTCTCTGC	901
Qy	901	TGGTGGCCACATGGGTGCTGTGGGAGGATCTATCTAATGTGGAGGCAGAAAGGATCA	960

Db	902	TGGTGGCCACATGGGTGCTGTGGGAGGATCTATCTAATGTGGAGGCAGAAAGGATCA	961
Qy	961	AGAAGACTTCTTTTCTACCAACCACTACTGCCCCCATTAAGGTCTTGTGGTTTACC	1020
Db	962	AGAAGACTTCTTTTCTACCAACCACTACTGCCCCCATTAAGGTCTTGTGGTTTACC	1021
Qy	1021	CATCTGAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTTCAAAACCAAT	1080
Db	1022	CATCTGAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTTCAAAACCAAT	1081
Qy	1081	GCAGAAGTGAAGTCTCTTGAAGAGTGGCAGAAAAGAAAATAGCAGAGATGGTCCAG	1140
Db	1082	GCAGAAGTGAAGTCTCTTGAAGAGTGGCAGAAAAGAAAATAGCAGAGATGGTCCAG	1141
Qy	1141	TGCAGTGGCTTGCCTCACTCAAAAGAGGAGCAGACAAAAGTCTCTCTTTTCCAATG	1200
Db	1142	TGCAGTGGCTTGCCTCACTCAAAAGAGGAGCAGACAAAAGTCTCTCTTTTCCAATG	1201
Qy	1201	ACGTCAACAGTGTGTGCGATGTACTCTGTGCAAGAGGAGGCGAGTCCCAAGTGAAC	1260
Db	1202	ACGTCAACAGTGTGTGCGATGTACTCTGTGCAAGAGGAGGCGAGTCCCAAGTGAAC	1261
Qy	1261	CTCAAGACCTTCTTCCCTTGAACCTTTTCTGAGTGTACTTAAGAGCCAGATTC	1320
Db	1262	CTCAAGACCTTCTTCCCTTGAACCTTTTCTGAGTGTACTTAAGAGCCAGATTC	1321
Qy	1321	ATCTGCACAAATACGTGTGTGTACTTTTAGAGAGATTGATACAAAGACGATTACAATG	1380
Db	1322	ATCTGCACAAATACGTGTGTGTACTTTTAGAGAGATTGATACAAAGACGATTACAATG	1381
Qy	1381	CTCTCAGTGTCTGCCCAAGTACCACTTTCATGAAGATGCCACTGCTTTTCTGTGAGAAC	1440
Db	1382	CTCTCAGTGTCTGCCCAAGTACCACTTTCATGAAGATGCCACTGCTTTTCTGTGAGAAC	1441
Qy	1441	TTCTCCATGTCAAGCAGCAGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1500
Db	1442	TTCTCCATGTCAAGCAGCAGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1501
Qy	1501	GCTGCTCTCTGTAG 1514	
Db	1502	GCTGCTCTCTGTAG 1515	

RESULT 15
 US-10-175-738-399
 ; Sequence 399, Application US/10175738
 ; Publication No. US20030022294A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Deanovers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C45
 ; CURRENT APPLICATION NUMBER: US/10175,738
 ; PRIORITY FILING DATE: 2002-06-19
 ; Prior application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 399
 ; LENGTH: 1515
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-175-738-399

Query Match		82.6%;	Score 1509.2;	DB 9;	Length 1515;
Best Local Similarity		99.8%;	Pred. No. 0;		
Matches 1511;		Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	CGGCGATGTCGCTCGTCTGATAAGCCTGGCGCGCTGTGCAGAGCGCGCTACCCCGAG	60		
Db	2	CGGCGATGTCGCTCGTCTGCTAAAGCCTGGCGCGCTGTGCAGAGCGCGCTACCCCGAG	61		
Qy	61	AGCGAGCGTTCAATGTGGCTCTGAACTGGGCGCATCTCAGAGTGGATGCTACAAATG	120		
Db	62	AGCGAGCGTTCAATGTGGCTCTGAACTGGGCGCATCTCAGAGTGGATGCTACAAATG	121		
Qy	121	ATCTAATCCCGAGACTTTGAGGACCTCCGAGTAGAACTGTACAACTAGTGTGCAA	180		
Db	122	ATCTAATCCCGAGACTTTGAGGACCTCCGAGTAGAACTGTACAACTAGTGTGCAA	181		
Qy	181	CAGGGGACTATTCAATTTTGAATGAATGTAAAGCTGGGTACTCCGGGCGAGATGCCAGCATCC	240		
Db	182	CAGGGGACTATTCAATTTTGAATGAATGTAAAGCTGGGTACTCCGGGCGAGATGCCAGCATCC	241		
Qy	241	GCTTGTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAATTTCCAGTCTCTACAGCT	300		
Db	242	GCTTGTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAATTTCCAGTCTCTACAGCT	301		
Qy	301	GTGTGAGGTGCAATTACACAGAGGCCCTCCAGACTCAGACCAGACCCCTCTGGTGGTAAT	360		
Db	302	GTGTGAGGTGCAATTACACAGAGGCCCTCCAGACTCAGACCAGACCCCTCTGGTGGTAAT	361		
Qy	361	GGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAAACAGCTATTTTCAATTGGGGCCC	420		
Db	362	GGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAAACAGCTATTTTCAATTGGGGCCC	421		
Qy	421	ATPATATTCCTAATGCAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACT	480		
Db	422	ATPATATTCCTAATGCAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACT	481		
Qy	481	CACCGGCTGCTAGACACATATGAATATATAAATAAAGTGTGCAAGGCGGAGGCC	540		
Db	482	CACCGGCTGCTAGACACATATGAATATATAAATAAAGTGTGCAAGGCGGAGGCC	541		
Qy	541	TGTGGGATCCGAACATCACTGTGTTGAAGAAGTGAAGAGAGAGTGAAGTGAACCTCA	600		
Db	542	TGTGGGATCCGAACATCACTGTGTTGAAGAAGTGAAGAGAGTGAAGTGAACCTCA	601		
Qy	601	CAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAAACACAGCACTATCATCGGT	660		
Db	602	CAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAAACACAGCACTATCATCGGT	661		
Qy	661	TTTCTCAGGTGTTGAGCCACACAGAGAAACAAACGGGAGCTTCAGTGGTGAATCCAG	720		
Db	662	TTTCTCAGGTGTTGAGCCACACAGAGAAACAAACGGGAGCTTCAGTGGTGAATCCAG	721		
Qy	721	TGACTGGGGATAGTGAAGTGTCTAGGTCAGCTGACTCCATATTTTCTACTTGTGGCA	780		
Db	722	TGACTGGGGATAGTGAAGTGTCTAGGTCAGCTGACTCCATATTTTCTACTTGTGGCA	781		
Qy	781	GGGACTGCATCCGACATAAAGGAACAGTTGTCTGTGCCCAACAAACAGGCGTCCCTTTCC	840		
Db	782	GGGACTGCATCCGACATAAAGGAACAGTTGTCTGTGCCCAACAAACAGGCGTCCCTTTCC	841		
Qy	841	CTCTGGATTAACAAACAAACAGCGGGAGGCTGGCTCTCTCTCTGTCTCTCTGC	900		
Db	842	CTCTGGATTAACAAACAAACAGCGGGAGGCTGGCTCTCTCTCTGTCTCTCTGC	901		
Qy	901	TGGTGCCACATGGGTGCTGGTGGAGGATCTATCTAATGTGGAGGACGAAAGGATCA	960		
Db	902	TGGTGCCACATGGGTGCTGGTGGAGGATCTATCTAATGTGGAGGACGAAAGGATCA	961		
Qy	961	AGAAGACTTCTTTTCTACCCACACTACTGCCGCCCAATTAAGGTTCTTGTGGTTTACC	1020		
Db	962	AGAAGACTTCTTTTCTACCCACCACTACTGCCGCCCAATTAAGGTTCTTGTGGTTTACC	1021		
Qy	1021	CATCTGAAATATGTTTCCATCAACAATTTGTACTTCACTGAAATTTCTTCAAAACCAATT	1080		

Db	1022	CATCTGAAATATGTTTCCATCAACAATTTGTTACTTCACTGAATTTCTTCAAAACCAATT	1081		
Qy	1081	GCAGAAGTGAGGTCTATCTTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAG	1140		
Db	1082	GCAGAAGTGAGGTCTATCTTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAG	1141		
Qy	1141	TGAGTGGCTTGGCACTCAAAAAGAGGAGCAGACAAAGTCGTCTCTCTTTTCCAATG	1200		
Db	1142	TGAGTGGCTTGGCACTCAAAAAGAGGAGCAGACAAAGTCGTCTCTCTTTTCCAATG	1201		
Qy	1201	AGTCAACAGCTGTGTGCGATGTGTGCGCAAGAGCGAGGCGAGTCCAGTGAGAACT	1260		
Db	1202	AGTCAACAGCTGTGTGCGATGTGTGCGCAAGAGCGAGGCGAGTCCAGTGAGAACT	1261		
Qy	1261	CTCAAGACCTTTCCTCCCTTTCCTTTTAACTTTTCTGCAGTGATCTTAAGAAGCCAGATTTC	1320		
Db	1262	CTCAAGACCTTTCCTCCCTTTCCTTTTAACTTTTCTGCAGTGATCTTAAGAAGCCAGATTTC	1321		
Qy	1321	ATCTGCAAAATACGTGGTGGTCTACTTTTAGAGAGATTGATACAAAAGACGATTACAATG	1380		
Db	1322	ATCTGCAAAATACGTGGTGGTCTACTTTTAGAGAGATTGATACAAAAGACGATTACAATG	1381		
Qy	1381	CTCTCAGTGTCTGCCCAAGTACCACCTCATGAAGATGCCACTGCTTTCTGTGCAGAAC	1440		
Db	1382	CTCTCAGTGTCTGCCCAAGTACCACCTCATGAAGATGCCACTGCTTTCTGTGCAGAAC	1441		
Qy	1441	TTCTCTCATGTCAAGCAGCAGGTGTGAGCAGGAAAAAGATCAAGCCTGCCACGATGGCT	1500		
Db	1442	TTCTCTCATGTCAAGCAGCAGGTGTGAGCAGGAAAAAGATCAAGCCTGCCACGATGGCT	1501		
Qy	1501	GCTGCTCTCTGTAG	1514		
Db	1502	GCTGCTCTCTGTAG	1515		

Search completed: May 28, 2003, 10:35:25
Job time : 219.956 secs

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	Matches	113;	Conservative	0;	Mismatches	105;	Indels	0;	Gaps	0
QY	1609	ACAAACAGCCTTAGTAATTAAACATTTTATCCCATATAAATTTCCAAATATTACTACT	1668							
Db	15455	AAAAAGAAAAATGAAATATATAAAAAAAATTTATTAATATATAAAAAA	15514							
QY	1669	AATGTAGCATTTACTACGATGGAACTACATTTACAACCTTCAAGCTGTTTATACAT	1728							
Db	15515	GGAGAAAAATTTTTTAAAAAATAATATAAATATATATAAATTTTCATGAAATA	15574							
QY	1729	AGAATTCATTTACACTTTAATTGAAACCTGAACATTTTATATGCAACATTAAGC	1788							
Db	15575	AAAAATGAAAAAGATTATCAAAAAAAATTTAAAAAATTTTATATATAAAAAATGA	15634							
QY	1789	ATCTTCCAAAAAATAAAAAAATAAAAAAATAAAAAA	1826							
Db	15635	TTATATAAAAAAATAAAAAACAAAGAGAAATAAAAAA	15672							

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1      RESULT 3
2      US-08-655-352-10
3      : Sequence 10, Application US/08655352
4      : Patent No. 6077991
5      : GENERAL INFORMATION:
6      : APPLICANT: Bachettira W. Poovaiah, Zhihua Liu,
7      : APPLICANT: Shameekumar Patil, Datsuke Takezawa
8      : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
9      : TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
10     : NUMBER OF SEQUENCES: 19
11     : CORRESPONDENCE ADDRESS:
12     : ADDRESSEE: Klarquist Sparkman Campbell Leigh &
13     : ADDRESSEE: Whinston, LLP
14     : STREET: One World Trade Center
15     : STREET: 121 S.W. Salmon Street
16     : STREET: Suite 1600
17     : CITY: Portland
18     : STATE: Oregon
19     : COUNTRY: United States of America
20     : ZIP: 97204
21     : COMPUTER READABLE FORM:
22     : MEDIUM TYPE: Disk, 3-1/2 inch
23     : COMPUTER: IBM PC compatible
24     : OPERATING SYSTEM: MS DOS
25     : SOFTWARE: Wordperfect 5.1
26     : CURRENT APPLICATION DATA:
27     : APPLICATION NUMBER: US/08/655,352
28     : FILING DATE:
29     : CLASSIFICATION: 800
30     : PRIOR APPLICATION DATA:
31     : APPLICATION NUMBER: 08/323,449
32     : FILING DATE: October 14, 1994
33     : ATTORNEY/AGENT INFORMATION:
34     : NAME: Dow, Alar. E.
35     : REGISTRATION NUMBER: 35,123
36     : REFERENCE/DOCKET NUMBER: 4630-45000
37     : TELECOMMUNICATION INFORMATION:
38     : TELEPHONE: (503) 226-7391
39     : TELEFAX: (503) 228-9446
40     : INFORMATION FOR SEQ. ID NO: 10:
41     : SEQUENCE CHARACTERISTICS:
42     : LENGTH: 1776 base pairs
43     : TYPE: nucleic acid
44     : STRANDEDNESS: double stranded
45     : TOPOLOGY: linear
46     : MOLECULE TYPE: cDNA to mRNA
47     : DESCRIPTION: Tobacco CCaMK cDNA and deduced amino-acid
48     : DESCRIPTION: sequence
49     : FEATURE:
50     : NAME/KEY: protein-coding sequence (not including
51     : NAME/KEY: stop codon)
52     : LOCATION: nucleotides 20-1570
53     : US-08-655-352-10

```

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Query Match 2.7%; Score 49.8; DB 3; Length 1776;
Best Local Similarity 66.1%; Pred. No. 0.0021;
Matches 72; Conservative 0; Mismatches 37; Indels 0; Gaps 0

Qy 1719 TTTATACATAGAAATTCATTACAGCTTTAATTGAAACCTGTACCATTTTGATATGCA 1778
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1668 TTTTATCACTACTCGTAAGAAAGATCTTTAAATTATTCGGAAGCTTTATGCTAATAAA 1727
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 1779 ACAATTAAGCATCTTCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1827
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1728 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1776
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
US-09-258-016-10
; Sequence 10, Application US/09258016
; Patent No. 6362395
; GENERAL INFORMATION:
; APPLICANT: Bachetti, W. Poovaiyah, Zhinua Liu,
; APPLICANT: Shameekumar Patil, Datsuke Takekawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klargquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,016
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephens Jr., Donald L.
; REGISTRATION NUMBER: 34,022
; REFERENCE/DOCKET NUMBER: 4630-51994
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1776 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; DESCRIPTION: Tobacco CCaMK cDNA and deduced amino-acid
; DESCRIPTION: sequence
; FEATURE:
; NAME/KEY: protein-coding sequence (not including
; NAME/KEY: stop codon)
; LOCATION: nucleotides 20-1570
; US-09-258-016-10

Query Match 2.7%; Score 49.8; DB 4; Length 1776;
Best Local Similarity 66.1%; Pred. No. 0.0021;
Matches 72; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 1719 TTTTATACATAGAAATTCATTACAGCTTTAATTGAAACCTGTACCATTTTGATATGCA 1778
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1668 TTTTATCACTACTCGTAAGAAAGATCTTTAAATTATTCGGAAGCTTTATGCTAATAAA 1727
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 1779 ACAATTAAGCATCTTCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1827
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1728 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1776
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 1728 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1776

RESULT 5
US-09-257-825B-10
; Sequence 10, Application US/09257825B
; Patent No. 640352
; GENERAL INFORMATION:
; APPLICANT: Poovaliah, Bachettira W.
; APPLICANT: Patil, Shameekumar
; APPLICANT: Takezawa, Daisuke
; TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
; FILE REFERENCE: 4630-51993
; CURRENT APPLICATION NUMBER: US/09/257, 825B
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: US 08/655,352
; PRIOR FILING DATE: 1996-05-23
; PRIOR APPLICATION NUMBER: US 60/014,743
; PRIOR FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-257-825B-10

Query March 2.7%; Score 49.8; DB 4; Length 1776;
Best Local Similarity 66.1%; Pred. No. 0.0021;
Matches 72; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 1719 TTTTATACATGAAATCAATTACAGCTTTAATTGAAAACTGTAAACATTTGATATGCA 1778
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1668 TTTTATACATCTACTGTAAAAAGATCCTTTAATTGATTCGAAACCTTTATGTAATAAA 1727
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 1779 ACAATTAAGCATCTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1827
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1728 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1776

RESULT 6
US-08-628-417-6
; Sequence 6, Application US/08628417
; Patent No. 5627054
; GENERAL INFORMATION:
; APPLICANT: GILLESPIE, DAVID
; TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
; ADDRESS: DEFENSE COMMAND
; STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
; CITY: ABERDEEN PROVING GROUND
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,417
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BIFFONI, ULYSSES J
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 398-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158

```

TELEFAX: 410-671-2534
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 240 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: oligodeoxynucleotide
 HYPOTHETICAL: NO
 ANTI-SENSE: YES
 US-08-628-417-6

Query Match 2.7%; Score 49.4; DB 1; Length 240;
 Best Local Similarity 51.6%; Pred. No. 0.0012;
 Matches 113; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 1609 ACAACGCTTGTATTAACATTTTATCCATTAATTTTCAATATTTACTACT 1668
 DB 6 ATAAAGCATTAATACTTTGAAATATTTTACTTAAAAAAAAAAAAAAAAAAAA 65
 QY 1669 AATGACATTAATACTGAACTCACTTCACTCACTGTTTATCAT 1728
 DB 66 AAA 125
 QY 1729 AGAATCAATTACAGCTTTATGAAACTGTACCATTTTGTATATGACATTAAGC 1788
 DB 126 AAA 185
 QY 1789 ATCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1827
 DB 186 AAA 224

RESULT 7
 US-07-861-458C-4
 Sequence 4, Application US/07861458C
 Patent No. 6232061
 GENERAL INFORMATION:
 APPLICANT: Marchionni, Mark Andrew
 TITLE OF INVENTION: HOMOLOGY CLONING
 NUMBER OF SEQUENCES: 142
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 502 or 555X
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/861,458C
 FILING DATE: 04/01/92
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 04585/014001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1100
 TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 US-07-861-458C-4

Query Match 2.7%; Score 49.2; DB 4; Length 1100;
 Best Local Similarity 73.3%; Pred. No. 0.0025;
 Matches 63; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1742 AGCTTAATTGAAACTGTAACCATTTGTATATGCAACATTAAGCATCTTCCAAAAA 1801
 DB 997 ATCTTAATTGTATATGAGAGCTTTTGTATTAATAAAAAAAAAAAAAAAAAAAAA 1056
 QY 1802 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1827
 DB 1057 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1082

RESULT 8
 US-08-747-221B-24
 Sequence 24, Application US/08747221B
 Patent No. 6063610
 GENERAL INFORMATION:
 APPLICANT: Silver, Gary W.
 TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 ADDRESSEE: Heeka Corporation
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/747, 221B
 FILING DATE: No. 6063610e1ember 12, 1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: FC-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2836 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 99..1889
 US-08-747-221B-24
 Query Match 2.7%; Score 49; DB 3; Length 2836;
 Best Local Similarity 58.6%; Pred. No. 0.0042;
 Matches 85; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1683 TAAGATTGAAACTGTAACCATTTGTATATGCAACATTAAGCATCTTCCAAAAA 1742
 DB 2688 TATGATTAATGTAACATGTAATTAACAAATGCGTTTAAATAATCTGTATTA 2747
 QY 1743 GCTTAATTGAAACTGTAACCATTTTGTATATGCAACATTAAGCATCTTCCAAAAA 1802

Db 2748 ATTGTTATATAAATCTGAAATGTAAGTCTTTAAGTAAAAA 2807
Oy 1803 AAAAAAAAAAAAAAAAAAAAAA 1827
Db 2808 AAAAAAAAAAAAAAAAAAAAAA 2832

RESULT 9

US-08-747-221B-26/c
Sequence 26, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610e1 December 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 2836 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-747-221B-26

Query Match 2.7%; Score 49; DB 3; Length 2836;

Best Local Similarity 58.6%; Pred. No. 0.0042; Mismatches 60; Indels 0; Gaps 0;
Matches 85; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Oy 1683 TAACATTGGAACCTGATTTCAACTTCAAGCTGTTTATATACATGAAATCAATTACA 1742
Db 149 TATGATTATATGTCACATGTAATACAAATGCGGTGTTAAAAATATCTGATTTAA 90
Oy 1743 GCTTAATTGAAACTGTACATTTGATTAATGCACATATAAGCATCTTCCAAAAA 1802
Db 89 ATTGTTATATAAATCTGAAATGTAAGTCTTTAAGTAAAAA 30
Oy 1803 AAAAAAAAAAAAAAAAAAAAAA 1827
Db 29 AAAAAAAAAAAAAAAAAAAAAA 5

RESULT 10
US-09-005-051-24
Sequence 24, Application US/09005051
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.

APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 629122e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 629122e1 December 12, 1996

ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2836 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 99..1889

US-09-005-051-24

Query Match 2.7%; Score 49; DB 4; Length 2836;

Best Local Similarity 58.6%; Pred. No. 0.0042; Mismatches 60; Indels 0; Gaps 0;
Matches 85; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Oy 1683 TAACATTGGAACCTGATTTCAACTTCAAGCTGTTTATATACATGAAATCAATTACA 1742
Db 2688 TATGATTATATGTCACATGTAATACAAATGCGGTGTTAAAAATATCTGATTTAA 2747
Oy 1743 GCTTAATTGAAACTGTACATTTGATTAATGCACATATAAGCATCTTCCAAAAA 1802
Db 2748 ATTGTTATATAAATCTGAAATGTAAGTCTTTAAGTAAAAA 2807
Oy 1803 AAAAAAAAAAAAAAAAAAAAAA 1827
Db 2808 AAAAAAAAAAAAAAAAAAAAAA 2832

RESULT 11
US-09-005-051-26/c
Sequence 26, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 629122e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/494-9505
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 2836 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-005-051-26

Query Match 2.7%; Score 49; DB 4; Length 2836;
Best Local Similarity 58.6%; Pred. No. 0.0042;
Matches 85; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1683 TAACGATTGAACTACATTACCACTTCAAGCTGTTTATACATAGAAATCAATTACA 1742
DB 149 TATGATTAATGTCACATGTAATAATCAAAATCGGTTTAAATAATCTGATTTAAA 90
QY 1743 GCTTAAATGAAACGTGAACCACTTTGATTAATGCACAAATAAGCATCTTCCAAAAA 1802
DB 89 ATGTATATATAAATCTGAATAATGACTTTTAAGTAAAAAATAAAAAATAAAAA 30
QY 1803 AAAAAAAAAAAAAAAAAAAAAAAAAA 1827
DB 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 12
US-08-242-677-1
Sequence 1, Application US/08242677
Patent No. 5677143
GENERAL INFORMATION:
APPLICANT: Gaynor, Richard B
APPLICANT: Wu, Foon W.
TITLE OF INVENTION: Cellular Nucleic Acid Binding Protein
TITLE OF INVENTION: and uses thereof in regulating Gene Expression and in the
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,677
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:401
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5173 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4863
US-08-242-677-1

Query Match 2.7%; Score 49; DB 1; Length 5173;
Best Local Similarity 69.1%; Pred. No. 0.0054;
Matches 67; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1731 AATCAATTACAGCCTTTAATGAAACCTGATTAATGATTAATGACATTAAGCAT 1790
DB 5059 AATTGATTTCTTCTTAATAAATTTTAAGCATTTGCTCAATTAATAAAAAAAAAA 5118
QY 1791 CTTCAAAAAAAAAAAAAAAAAAAAAAAAA 1827
DB 5119 AAAAAAAAAAAAAAAAAAAAAAAAAA 5155

RESULT 13
US-09-014-969-14
Sequence 14, Application US/09014969
Patent No. 5965397
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Werberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Springer, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284

TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-014-969-14

Query Match 2.6%; Score 48.4; DB 2; Length 2447;
Best Local Similarity 50.4%; Pred. No. 0.0056;
Matches 118; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1594 CTTACTATGACGCTTCAACAGCCTTAGTAATTAACATTTTATACCAATTAATTTT 1653
DB 2214 CTTTAATGTGCAATTAACCTTTGGGAGAAAAAATTTTATTTTATTTTATTTT 2273
QY 1654 CAATATTCTAATCTAGTACATTAACTAAGATTGGAATCACTTACCACTTCAA 1713
DB 2274 AA 2333
QY 1714 AGCTGTTTATCATGAAATCAATACGCTTTATTTGAAAACGTACCACTTTGATA 1773
DB 2334 AA 2393
QY 1774 ATGCACAAATTAAGCATCTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1827
DB 2394 AA 2447

RESULT 14

US-08-924-747-25
Sequence 25, Application US/08924747
Patent No. 6063570

GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
TITLE OF INVENTION: ENZYMES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924.747
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AKAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL-1108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 991 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
TISSUE TYPE: SOYBEAN
IMMEDIATE SOURCE:
CLONE: SSM.PK0067.G5
US-08-924-747-25

Query Match 2.6%; Score 48.2; DB 3; Length 991;
Best Local Similarity 69.9%; Pred. No. 0.0043;
Matches 65; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1735 CAATTACAGCTTAAATGAAAGCTGAACCACTTTGATATGCAACAATTAAGCATCTTC 1794
DB 891 CTAATTTAATTTAATCAATAAAGAGTTCAGTTTAAAAAATTTTAAAAA 950
QY 1795 CAAA 1827
DB 951 AA 983

RESULT 15

US-09-247-373B-25
Sequence 25, Application US/09247373B
Patent No. 6168954

GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-B
CURRENT APPLICATION NUMBER: US/09/247.373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924.747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
LENGTH: 991
TYPE: DNA
ORGANISM: SOYBEAN
US-09-247-373B-25

Query Match 2.6%; Score 48.2; DB 4; Length 991;
Best Local Similarity 69.9%; Pred. No. 0.0043;
Matches 65; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1735 CAATTACAGCTTAAATGAAAGCTGAACCACTTTGATATGCAACAATTAAGCATCTTC 1794
DB 891 CTAATTTAATTTAATCAATAAAGAGTTCAGTTTAAAAAATTTTAAAAA 950
QY 1795 CAAA 1827
DB 951 AA 983

Search completed: May 28, 2003, 10:19:18
Job time: 165.735 secs

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XX 04-FEB-2000; 2000US-0180374.
 PR (UYAR-) UNIV ARKANSAS.
 PA Shaughnessy JD;
 XX MPI; 2001-496920/54.
 DR P-PSDB; AAE07160.
 XX New nucleic acids encoding an interleukin (IL)-17 receptor related
 PT protein for use as a marker for leukemia -
 PS Claim 1a; Page 74-75; 87pp; English.
 XX The present sequence is a cDNA encoding human interleukin (IL)-17
 CC receptor related protein (Evi27). Human Evi27 gene was mapped to
 CC chromosome 3p21. Evi27 is a common site of retroviral integration
 CC in BKH2 murine myeloid leukaemias. Evi27 cDNA sequences are useful
 CC as antisense molecules to inhibit Evi27 protein or for chromosomal
 CC mapping or mutational analysis of Evi27 protein. They are proviral
 CC integration sites associated with leukaemias and monitoring this
 CC site provides a genetic tag for disease gene identification. The
 CC proteins of the invention are useful to stimulate the secretion of
 CC proinflammatory cytokines such as IL-8 and plays an important role
 CC in the developmental and/or disease processes of haematopoietic
 CC cells. Hence modulating the expression of Evi27 at the RNA or
 CC protein level is used in the treatment of diseases such as cancer
 CC or autoimmune diseases.
 XX Sequence 1827 BP; 547 A; 438 C; 397 G; 445 T; 0 other;
 SQ
 Query Match 100.0%; Score 1827; DB 22; Length 1827;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 541 TGTGGATCCGAACATCTGCTTGTAAAGAAATGAGAGACAGTAAAGTAACTTCA 600
 QY CAACCACTCCCTCGGAAAAGATACATGCTCTTATCCAAACAGACATATCATCGGCT 660
 QY 601 CAACCACTCCCTCGGAAAAGATACATGCTCTTATCCAAACAGACATATCATCGGCT 660
 Db 601 CAACCACTCCCTCGGAAAAGATACATGCTCTTATCCAAACAGACATATCATCGGCT 660
 QY 661 TTTCTCAGGTGTTTGAACCAACAGAGAAAACAAACGAGCTTCAAGTGTATCCAG 720
 Db 661 TTTCTCAGGTGTTTGAACCAACAGAGAAAACAAACGAGCTTCAAGTGTATCCAG 720
 QY 721 TGAATGGGATATGAGAGTGTCTACGCTGACGTGACTGATATTTTCTACTTGTGGCA 780
 Db 721 TGAATGGGATATGAGAGTGTCTACGCTGACGTGACTGATATTTTCTACTTGTGGCA 780
 QY 781 GGCATGTCATCCGACATAAAGGAAAGTGTGCTGACCAACAAACAGGCTCCCTTCC 840
 Db 781 GGCATGTCATCCGACATAAAGGAAAGTGTGCTGACCAACAAACAGGCTCCCTTCC 840
 QY 841 CTCTGGATTAACAACAAAGCAAGCCGGAAGGCTGCTGCTCTCTGCTGTCTTGC 900
 Db 841 CTCTGGATTAACAACAAAGCAAGCCGGAAGGCTGCTGCTCTCTGCTGTCTTGC 900
 QY 901 TGTGGCCACATGGGTGCTGTGGCAGGGAATCTATCTAATGTGAGGCAAGAAAGATCA 960
 Db 901 TGTGGCCACATGGGTGCTGTGGCAGGGAATCTATCTAATGTGAGGCAAGAAAGATCA 960
 QY 961 AGAAGACTTCTTTTCTACCAACACACTGCCCCCTTAAGTCTTGTGTTTACC 1020
 Db 961 AGAAGACTTCTTTTCTACCAACACACTGCCCCCTTAAGTCTTGTGTTTACC 1020
 QY 1021 CATCTGAATATATGTTTCAATCAACAAATTTGTACTTCACTGAATTTCTTCAAAACATT 1080
 Db 1021 CATCTGAATATATGTTTCAATCAACAAATTTGTACTTCACTGAATTTCTTCAAAACATT 1080
 QY 1081 GCAGAAGTAAAGTCTCTTGAAGAAAGTGGCAGAAAATACAGAGATGGGTCCAG 1140
 Db 1081 GCAGAAGTAAAGTCTCTTGAAGAAAGTGGCAGAAAATACAGAGATGGGTCCAG 1140
 QY 1141 TGCAGTGGCTTGCACACTCAAAAGAGGAGCAGCAAAAGTGTCTTCTTCTTCAATG 1200
 Db 1141 TGCAGTGGCTTGCACACTCAAAAGAGGAGCAGCAAAAGTGTCTTCTTCTTCAATG 1200
 QY 1201 ACGTCAACAGTGTGTCAGATGCTGTGACCTGTGGCAGAGGAGGAGTCCAGTGAAT 1260
 Db 1201 ACGTCAACAGTGTGTCAGATGCTGTGACCTGTGGCAGAGGAGGAGTCCAGTGAAT 1260
 QY 1261 CTCAAGACCTCTTCCCTTGGCTTTAACTTTTCTGCAATGATCTTAAGAACAGATTTC 1320
 Db 1261 CTCAAGACCTCTTCCCTTGGCTTTAACTTTTCTGCAATGATCTTAAGAACAGATTTC 1320
 QY 1321 ATCTGCAAAATACGAGTGTGCTACTTGAAGATGATCAAAAGACATTAATG 1380
 Db 1321 ATCTGCAAAATACGAGTGTGCTACTTGAAGATGATCAAAAGACATTAATG 1380
 QY 1381 CTCTCAGTGTCTGCCCCAAGTACACTTCAATGAGATGCCACTTCTGTGCAAGAC 1440
 Db 1381 CTCTCAGTGTCTGCCCCAAGTACACTTCAATGAGATGCCACTTCTGTGCAAGAC 1440
 QY 1441 TTCTCATGTCAAGCAGCAGGTGTGAGCAGAGAAAAGATCACAGCTTGCAGTGGCT 1500
 Db 1441 TTCTCATGTCAAGCAGCAGGTGTGAGCAGAGAAAAGATCACAGCTTGCAGTGGCT 1500
 QY 1501 GGTGCTCTCTGAGCCACCAATGAGAGCAAGACCTTAAAGCTTCTATCCACACA 1560
 Db 1501 GGTGCTCTCTGAGCCACCAATGAGAGCAAGACCTTAAAGCTTCTATCCACACA 1560
 QY 1561 ATTACAGGAGAAAAGATGTGATGATCTGAAGCTTACTATGAGCCTTCAAAACAGCTT 1620
 Db 1561 ATTACAGGAGAAAAGATGTGATGATCTGAAGCTTACTATGAGCCTTCAAAACAGCTT 1620
 QY 1621 AGTAATTAACAATTTTATCAATTAATTTTCAATATTTCTAATGATGATGATTA 1680

Db 1621 AGTAATTAACCTTTATACCAATATAATTTCAAAATTTACTATCACTATGATGACATTA 1680
 Qy 1681 ACTAGCATTTGGAACATACATTTTACCACTTCAAGCTGTTTATACATGAAATCAATTA 1740
 Db 1681 ACTAGCATTTGGAACATACATTTTACCACTTCAAGCTGTTTATACATGAAATCAATTA 1740
 Qy 1741 CAGCTTAATTTGAAAACCTGTACCATTTTGTATATGCAACATTAAGCATTTTCCAAAA 1800
 Db 1741 CAGCTTAATTTGAAAACCTGTACCATTTTGTATATGCAACATTAAGCATTTTCCAAAA 1800
 Qy 1801 AAAAAAAAAAAAAAAAAAAAAAAAAA 1827
 Db 1801 AAAAAAAAAAAAAAAAAAAAAAAAAA 1827
 RESULT 2
 AAD28776
 ID AAD28776 standard; DNA; 1841 BP.
 AC AAD28776;
 XX
 DT 07-MAY-2002 (first entry)
 XX
 DE Human Interleukin-17 receptor B-2 (IL-17RB-2) DNA.
 XX
 KW Human; interleukin-17 receptor B-2; IL-17RB-2; immune system dysfunction;
 KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;
 KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;
 KW autoimmune disorder; lung; skin; kidney; bone; eye; glomerulonephritis;
 KW infection; hepatitis; obesity; anorexia; cachexia; vascular system;
 KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;
 KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;
 KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;
 KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;
 KW cancer; diabetes; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 50..1558
 FT /*tag= a
 FT /product= "Human IL-17RB-2 protein"
 FT sig_peptide 50..92
 FT /*tag= b
 FT mat_peptide 93..1555
 FT /*tag= c
 FT /product= "Mature IL-17RB-2 protein"
 FT
 PN WO200208285-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 21-JUN-2001; 2001WO-US19861.
 XX
 PR 22-JUN-2000; 2000US-213125P.
 PR 02-FEB-2001; 2001US-266159P.
 PR 16-MAR-2001; 2001US-0810384.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;
 XX
 DR MPI; 2002-155217/20.
 DR P-PSDB; AAE16127.
 XX
 PT Nucleic acid molecules encoding Interleukin 17 (IL-17) - like
 PT polypeptides useful in the treatment, prevention and diagnosis of
 PT diseases e.g. cancer
 XX
 PS Disclosure; Page 230-232; 242pp; English.
 XX
 CC The invention relates to nucleic acid molecules encoding Interleukin 17
 CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels

CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,
 CC preventing or ameliorating a disease, such as immune system dysfunction
 CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease);
 CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel
 CC disease, transplant rejection, graft vs. host disease); infections (HIV,
 CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,
 CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung
 CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin
 CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone
 CC (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy
 CC atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma
 CC leukaemia); reproductive (infertility, miscarriage, endometriosis), eye
 CC (blindness, retinal neuropathy) and treatment of diseases involving
 CC inflammation. The present sequence is human Interleukin-17 receptor B-2
 CC (IL-17RB-2) DNA.
 XX
 SQ Sequence 1841 BP; 522 A; 455 C; 416 G; 448 T; 0 other;
 XX
 Query Match 97.8%; Score 1786; DB 24; Length 1841;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1789; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CGGCATGTCGTCGCTGATTAACCTTGGCCGCGCTGTGACGAGCCGCCAATCCCGG 60
 Db 45 CGGCATGTCGTCGCTGCTTAAACCTTGGCCGCGCTGTGACGAGCCGCCAATCCCGG 104
 Qy 61 AGCCACCGTTAATGTTGGCTCTGAAACTGGGCGCATCTCCAGTGGATGATCAACATG 120
 Db 105 AGCCACCGTTAATGTTGGCTCTGAAACTGGGCGCATCTCCAGTGGATGATCAACATG 164
 Qy 121 ATCTAATCCCGGAGACTTGAAGGACCTCGAGTAAACCTGTTACAACTAGTGTGCA 180
 Db 165 ATCTAATCCCGGAGACTTGAAGGACCTCGAGTAAACCTGTTACAACTAGTGTGCA 224
 Qy 181 CAGGGACTATTCATTTTGAATGAATGAAGTGGTCTCCGGGCAATGCGACATTC 240
 Db 225 CAGGGACTATTCATTTTGAATGAATGAAGTGGTCTCCGGGCAATGCGACATTC 284
 Qy 241 GCTTGTGAAGGCCACCAAGATTTGTGACGGGCAAAAGCAATCTCAGTCCCTACAGT 300
 Db 285 GCTTGTGAAGGCCACCAAGATTTGTGACGGGCAAAAGCAATCTCAGTCCCTACAGT 344
 Qy 301 GTGTAGGTGCAATTACACAGAGGCTTCCAGACTCAGACCGCTCTGGTGGTAAT 360
 Db 345 GTGTAGGTGCAATTACACAGAGGCTTCCAGACTCAGACCGCTCTGGTGGTAAT 404
 Qy 361 GGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACAAGCTATTTCAATGGGCCC 420
 Db 405 GGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACAAGCTATTTCAATGGGCCC 464
 Qy 421 ATATATTCCTAATGCAATATGAATGAATGAGGCTTCCATGCTGTGAATTCACCT 480
 Db 465 ATATATTCCTAATGCAATATGAATGAATGAGGCTTCCATGCTGTGAATTCACCT 524
 Qy 481 CACCAAGCTGCTTGAACACATATGAATATTAATAAAGTGTCAAGGCCGGAAGCC 540
 Db 525 CACCAAGCTGCTTGAACACATATGAATATTAATAAAGTGTCAAGGCCGGAAGCC 584
 Qy 541 TGTGGATCCGAACATCACTGCTGTGAAGATGAGAGACAGTAGAAGTAACTTCA 600
 Db 585 TGTGGATCCGAACATCACTGCTGTGAAGATGAGAGACAGTAGAAGTAACTTCA 644
 Qy 601 CAACACATCCCTGGGAAACAGATACATGCTTTATCCACACAGCACTATCATCGGGT 660
 Db 645 CAACACATCCCTGGGAAACAGATACATGCTTTATCCACACAGCACTATCATCGGGT 704
 Qy 661 TTTCTCAGGTGTTTGAAGCACACGAAAGAAACAAACCGAGCTTCACTGTGATTCAG 720
 Db 705 TTTCTCAGGTGTTTGAAGCACACGAAAGAAACAAACCGAGCTTCACTGTGATTCAG 764
 Qy 721 TGACTGGGATAGTGAAGGTGCTACGCTGACCTGATCTATTTTCTACTTGTGCA 780
 Db 765 TGACTGGGATAGTGAAGGTGCTACGCTGACCTGATCTATTTTCTACTTGTGCA 824

[illegible]

Db	1245	ACGTAAACAGATGTGTGGCATGGTACTGTGGCAAGACGAGGGCAGATGCCAGTGAAGAACT	1304
Qy	1261	CTCAAGACCTCTTCCCTCCCTTGAACCTTTTCTGCAGTATCTAAGAACCCAGATTC	1320
Db	1305	CTCAAGACCTCTTCCCTCCCTTGAACCTTTTCTGCAGTATCTAAGAACCCAGATTC	1364
Qy	1321	ATCTGCACAAATACGTGGTGGTCTACTTCTTAGAGGATTTGATACAAAGACGATTACATG	1380
Db	1365	ATCTGCACAAATACGTGGTGGTCTACTTCTTAGAGGATTTGATACAAAGACGATTACATG	1424
Qy	1381	CTCTCAGTGTGCGCCCAAGTACCACTTATGAGAGATGGCCACGCTTCTGTGCAGAAC	1440
Db	1425	CTCTCAGTGTGCGCCCAAGTACCACTTATGAGAGATGGCCACGCTTCTGTGCAGAAC	1484
Qy	1441	TTCTTCATGTCAAGCAGCAGGTGTCAAGCAGAAAAAGATCAACAAGCTGCACGATGGCT	1500
Db	1485	TTCTTCATGTCAAGCAGCAGGTGTCAAGCAGAAAAAGATCAACAAGCTGCACGATGGCT	1544
Qy	1501	GCTGCTCCTTGTAGCCCAACCATAGAGACAGACCTTAAAGGCTTCTATCCACCA	1560
Db	1545	GCTGCTCCTTGTAGCCCAACCATAGAGACAGACCTTAAAGGCTTCTATCCACCA	1604
Qy	1561	ATTACAGGAAAAAAGCGTATGATCTGTAAGCTTACTATGACGCTTACAAACAGCCTT	1620
Db	1605	ATTACAGGAAAAAAGCGTATGATCTGTAAGCTTACTATGACGCTTACAAACAGCCTT	1664
Qy	1621	AGTAATTTAAAAATTATTAACCAATPAAATTTCAAAATATTACTAATTAATGTAGCATTA	1680
Db	1665	AGTAATTTAAAAATTATTAACCAATPAAATTTCAAAATATTACTAATTAATGTAGCATTA	1724
Qy	1681	ACTTAACAGTTGGAAAATCTACATTATCAAACTTCAAAAGCTGTTTATATACATAGAAATCAATTA	1740
Db	1725	ACTTAACAGTTGGAAAATCTACATTATCAAACTTCAAAAGCTGTTTATATACATAGAAATCAATTA	1784
Qy	1741	CAGCTTTAATTGAAAACTGTAAACATTTGATATGCAACATTAACATCCTTC	1794
Db	1785	CAGCTTTAATTGAAAACTGTAAACATTTGATATGCAACATTAACATCCTTC	1838
RESULT 4			
AAS18126			
ID	AAS18126 standard; cDNA; 1796 BP.		
XX			
AC	AAS18126;		
XX			
DT	26-MAR-2002 (first entry)		
XX			
DE	Human DNAX cytokine receptor subunit 6 (DCRS6) cDNA.		
XX			
KW	Human; DNAX cytokine receptor subunit 6; DCRS6; phosphate labelling; ss;		
XX	gene therapy; protein therapy; immunological disorder.		
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FT	4..1512		
FT	/*tag= a		
FT	/product= "Human DCRS6"		
XX			
PN	WO200190358-A2.		
XX			
PD	29-NOV-2001.		
XX			
PF	23-MAY-2001; 2001WO-US16767.		
XX			
PR	24-MAY-2000; 2000US-206862P.		
XX			
PA	(SCHE) SCHERING CORP.		
XX			
PI	Gorman DM;		
XX			
DR	WPI; 2002-106198/14.		

DR P-PSDB; AAU11351.
 XX Isolated antigenic human or mouse DNA receptor subunit-like
 PT polypeptide useful for detecting antibodies generated in response to
 PT presence of increased protein levels or immunological disorders -
 XX
 XX Disclosure; Page 7-10; 148bp; English.
 XX
 CC The invention relates to primate and rodent DNA cytokine receptor
 CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
 CC receptors, or their portions may be useful as phosphate labelling enzymes
 CC to label general or specific substrates. The subunits may also be
 CC functional immunogens to elicit recognising antibodies, or antigens
 CC capable of binding antibodies. A combination, e.g., including a DCRS can
 CC be used as an immunogen for the production of antisera or antibodies
 CC capable of distinguishing between other cytokine receptor family members.
 CC A purified DCRS can also be used as a reagent to detect antibodies
 CC generated in response to the presence of elevated levels of expression,
 CC or immunological disorders which lead to antibody production to the
 CC endogenous receptor. This sequence represents cDNA encoding the human
 CC DCRS6 polypeptide.
 CC
 SO Sequence 1796 BP; 514 A; 439 C; 399 G; 444 T; 0 other;
 Query Match 97.7%; Score 1785.6; DB 24; Length 1796;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1788; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 661 TCTCAGGTGTTTGAAGCAACAGAAAGAAACAAACCGAGCTTCACTGGATTCAGTG 720
 QY 723 ACTGGGATATGTAAAGTGTAGTGCAGTCACTATATTTTCTACTTGTGCAGC 782
 Db 721 ACTGGGATATGTAAAGTGTAGTGCAGTCACTATATTTTCTACTTGTGCAGC 780
 QY 783 GACTGCATCCGACATTAAGGAACAGTTGTGCTGCGCCAAACAGAGCGCTTCCCT 842
 Db 781 GATTCATCCGACATTAAGGAACAGTTGTGCTGCGCCAAACAGAGCGCTTCCCT 840
 QY 843 CTGGATTAACAACAAAGCAAGCGGAGGCTGCTCTCTCTCTCTCTCTCTCTCTG 902
 Db 841 CTGGATTAACAACAAAGCAAGCGGAGGCTGCTCTCTCTCTCTCTCTCTCTCTG 900
 QY 903 GTGGCCACATGGGTGTGGTGGTGGAGGATCTATATATGTAGAGGACGAAAGATCAAG 962
 Db 901 GTGGCCACATGGGTGTGGTGGTGGAGGATCTATATATGTAGAGGACGAAAGATCAAG 960
 QY 963 AAGACTTCTCTTCTACACACACACTACTGCCCATTAAGGTTCTTGTGTTTACCA 1022
 Db 961 AAGACTTCTCTTCTACACACACACTACTGCCCATTAAGGTTCTTGTGTTTACCA 1020
 QY 1023 TCTGAATATGTTTTCATCAACAATTTGTATCTTCACTGAATTTCTTCAAAACCA 1082
 Db 1021 TCTGAATATGTTTTCATCAACAATTTGTATCTTCACTGAATTTCTTCAAAACCA 1080
 QY 1083 AGAAGTAGGTATCTCTTGAAGAGTGGCAAGAAATAGCAGAGTGGTCCAGTG 1142
 Db 1081 AGAAGTAGGTATCTCTTGAAGAGTGGCAAGAAATAGCAGAGTGGTCCAGTG 1140
 QY 1143 CAGTGCCTTGCACCTCAAAAGAGGACAGACAAAGTGGTCTTCTTCAATGAC 1202
 Db 1141 CAGTGCCTTGCACCTCAAAAGAGGACAGACAAAGTGGTCTTCTTCAATGAC 1200
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 Db 1201 GTCAACAGTGTGCGAGTGTACTGTGGCAAGGAGGAGTCCAGTAGAACTCT 1260
 QY 1263 CAAGACTCTTCCCTCCCTTAACTTTCTGAGGATCTAAGAACCAAGATTCAT 1322
 Db 1261 CAAGACTCTTCCCTCCCTTAACTTTCTGAGGATCTAAGAACCAAGATTCAT 1320
 QY 1323 CTGCACAAATAGGTGTGTACTTTAGAGATTTGATACAAAGACGATTACATGCT 1382
 Db 1321 CTGCACAAATAGGTGTGTACTTTAGAGATTTGATACAAAGACGATTACATGCT 1380
 QY 1383 CTGAGTGTGCCCCCAAGTACCTTATGAAGATGCCACTGCTTTGTGCAAACTT 1442
 Db 1381 CTGAGTGTGCCCCCAAGTACCTTATGAAGATGCCACTGCTTTGTGCAAACTT 1440
 QY 1443 CTGCATGTCAACAGAGGTGTACAGAGAAATGATCAAGCCGTCGACAGATGGCTGC 1502
 Db 1441 CTGCATGTCAACAGAGGTGTACAGAGAAATGATCAAGCCGTCGACAGATGGCTGC 1500
 QY 1503 TGCTCTTGTAGCCACCATGAGAGCAAGACCTTAAAGGCTTCTCATCCCAAT 1562
 Db 1501 TGCTCTTGTAGCCACCATGAGAGCAAGACCTTAAAGGCTTCTCATCCCAAT 1560
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 Db 1561 TACAGGAAAAAAGCGTGATGATCTGAAGCTTATCTATGACGCTACAAACAGCTTAG 1620
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 QY 1683 TAACATTTGAACATTAATTTCAACTTCAAGGCTTTTATACATAGAAATCAATACA 1742
 Db 1681 TAACATTTGAACATTAATTTCAACTTCAAGGCTTTTATACATAGAAATCAATACA 1740
 QY 1743 GCTTTAATTTGAACATTTTATGATGATGATGATGATGATGATGATGATGATGATG 1794

KM resistant chronic infection; acute infection; mycobacterial infection;
 KM T-cell proliferation; IL-2 biosynthesis; lymphocytic leukemia;
 KM T-cell mediated autoimmune disease; hematopoiesis; sepsis; hybridoma;
 KM IL-6 expression; myeloma; plasmacytoma; Lennert's lymphoma;
 KM immunoprotective; cytostatic; hematopoietic; proliferative;
 KM antibacterial; ss.

OS Homo sapiens.

Key Location/Qualifiers
 CDS 111..1412

FT /tag= a
 FT /product= "Interleukin-17 like receptor protein"

PN WO200015759-A1.

PD 23-MAR-2000.

PF 15-SEP-1999; 99WO-US21048.

PR 16-SEP-1998; 98US-0154219.

PR 16-SEP-1998; 98WO-US19121.

PR 16-MAR-1999; 99US-0268311.

PA (HUMA-1) HUMAN GENOME SCI INC.

PI Ruben SM, Shi Y;

DR MPI: 2000-271403/23.

DR P-85DB; AAY70595.

PT Novel polynucleotides encoding interleukin-17-like receptor protein,
 PT useful for diagnosis and treatment of immune system-related disorders,
 PT e.g. sepsis and cancers -

PS Disclosure: Page 141-143; 147pp; English.

XX The patent relates to novel interleukin-17-like receptor
 CC protein (IL-17RLP). IL-17RLP is a homologue of the IL-17 receptor and has
 CC a wide range of cytokine receptor-like activities. IL-17RLP or its
 CC agonists may be used to enhance host defenses against resistant chronic
 CC and acute infections, e.g. mycobacterial infections, via the attraction
 CC and activation of microbicidal leukocytes. It may also be used to
 CC increase T-cell proliferation by stimulating IL-2 biosynthesis, for the
 CC treatment of T-cell mediated autoimmune diseases and lymphocytic
 CC leukaemias. IL-17RLP may also be used to regulate hematopoiesis and to
 CC treat sepsis. Extracellular IL-17RLP domains may be used as antagonists
 CC of IL-17RLP. IL-17RLP agonists and antagonists can also be used to
 CC modulate IL-6 expression, useful in treatment of cancers such as
 CC myelomas, plasmacytomas and hybridomas and Lennert's lymphoma. The
 CC present cDNA sequence encodes human IL-17RLP. This cDNA sequence was
 CC derived from sequencing the HAPOR40 cDNA clone (ATCC deposit
 CC number: 209198)

XX Sequence 1918 BP; 560 A; 469 C; 426 G; 461 T; 2 other;

Query Match 97.6%; Score 1782.4; DB 21; Length 1918;

Best Local Similarity 99.3%; Pred. No. 0; Mismatches 11; Indels 1; Gaps 1;

Matches 1800; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 3 GCGATGTCGTCGTGTGTAAGCTGCGCGGCTGTGAGAGAGCGCCGATCCCGAGAG 62
 DB 108 GCGATGTCGTCGTGTGTAAGCTGCGCGGCTGTGAGAGAGCGCCGATCCCGAGAG 167
 QY 63 CCGACCGTTCATGTGCTGTGTAAGCTGCGCGGCTGTGAGAGAGCGCCGATCCCGAGAG 122
 DB 168 CCGACCGTTCATGTGCTGTGTAAGCTGCGCGGCTGTGAGAGAGCGCCGATCCCGAGAG 227
 QY 123 CTAATCCCGAGAGCTTGAGAGAGCTTCGAGAGAGAGCTGTATCAACTAGTGTGCAACA 182
 DB 228 CTAATCCCGAGAGCTTGAGAGAGCTTCGAGAGAGAGCTGTATCAACTAGTGTGCAACA 287
 QY 183 GGGGACTATTCATTTGATGATGTAAGCTGGGATCTCCGCGGAGATGCCAGATCCGC 242

DB 288 GGGGACTATTCATTTGATGATGTAAGCTGGGATCTCCGCGGAGATGCCAGATCCGC 347
 QY 243 TTGTTGAAGGCGACCAAGATTTGTGTGA CCGGCAAAAGCACTTCCAGCTCCACAGCTGT 302
 DB 348 TTGTTGAAGGCGACCAAGATTTGTGTGA CCGGCAAAAGCACTTCCAGCTCCACAGCTGT 407
 QY 303 GTGAGTGTGCAATTAACAGAGAGCTTCCAGACTCAGACAGACCTCTGTGTGAATG 362
 DB 408 GTGAGTGTGCAATTAACAGAGAGCTTCCAGACTCAGACAGACCTCTGTGTGAATG 467
 QY 363 ACATTTTCCATATATGCGCTTCCCTGTGAGAGCTGAACACAGCTATTTTCAATGGGCCCAT 422
 DB 468 ACATTTTCCATATATGCGCTTCCCTGTGAGAGCTGAACACAGCTATTTTCAATGGGCCCAT 527
 QY 423 AATATTCCTAATGCAAAATGTAATGAATGAGGCCCTTCCAGACTCAGTGAATTCACCTCA 482
 DB 528 AATATTCCTAATGCAAAATGTAATGAATGAGGCCCTTCCAGACTCAGTGAATTCACCTCA 587
 QY 483 CCAGGCTGCTAGACCAATATATTAATAAAGTGTGCAAGCCGGAAGCCTG 542
 DB 588 CCAGGCTGCTAGACCAATATATTAATAAAGTGTGCAAGCCGGAAGCCTG 647
 QY 543 TGGATCCGAAATGATGCTGTTGTAAGAAATGAGAGACGTAAGAGTGAACCTTACA 602
 DB 648 TGGATCCGAAATGATGCTGTTGTAAGAAATGAGAGACGTAAGAGTGAACCTTACA 707
 QY 603 ACCATCCCTGCGGAAACAGATATACAGTCTCTATCCAAACAGACATATCATCGGGTTT 662
 DB 708 ACCATCCCTGCGGAAACAGATATACAGTCTCTATCCAAACAGACATATCATCGGGTTT 767
 QY 663 TCTCAGTGTGTTGAGCCACACAGAGAAACAAAGCGAGCTTCAGTGTGATTCAGTG 722
 DB 768 TCTCAGTGTGTTGAGCCACACAGAGAAACAAAGCGAGCTTCAGTGTGATTCAGTG 827
 QY 723 ACTGGGATAGTAAAGTGCTACAGGTGAGCTGACTCCATATTTTCCATCTTGCGACG 782
 DB 828 ACTGGGATAGTAAAGTGCTACAGGTGAGCTGACTCCATATTTTCCATCTTGCGACG 887
 QY 783 GACTGCATCCGACATTAAGAAAGCAAGTTGTGCTGTCGCCCAAAAGCGGTCCTTTCCCT 842
 DB 888 GACTGCATCCGACATTAAGAAAGCAAGTTGTGCTGTCGCCCAAAAGCGGTCCTTTCCCT 947
 QY 843 CTGATTAACAACAAAGAGAGCGGAGAGCTGAGCTGCTCTCTCTGCTGTGCTG 902
 DB 948 CTGATTAACAACAAAGAGAGCGGAGAGCTGAGCTGCTCTCTCTGCTGTGCTG 1007
 QY 903 GTGGCAGATGGGTGCTGTGAGAGAGATCTATATGTGAGGACAGAAAGATCAAG 962
 DB 1008 GTGGCAGATGGGTGCTGTGAGAGAGATCTATATGTGAGGACAGAAAGATCAAG 1067
 QY 963 AAGATTCCTTTTCTACACCACTACTGCCCCCATTAAGTGTGTGTGTTACCA 1022
 DB 1068 AAGATTCCTTTTCTACACCACTACTGCCCCCATTAAGTGTGTGTGTTACCA 1127
 QY 1023 TCTGAATATATGTTTCCATCACAATTTGTACTTCACTGAATTTCTCAAAACCATATGC 1082
 DB 1128 TCTGAATATATGTTTCCATCACAATTTGTACTTCACTGAATTTCTCAAAACCATATGC 1187
 QY 1083 AGAAGTGAAGTCACTCTTGAAGAGTGGCAGAAAGAAATAGCAGAGATGGTCCAGTG 1142
 DB 1188 AGAAGTGAAGTCACTCTTGAAGAGTGGCAGAAAGAAATAGCAGAGATGGTCCAGTG 1247
 QY 1143 CAGTGTGCTGCACTCAAAAGAGGACAGACAAAGTGTCTCTCTCTTCCAAATAC 1202
 DB 1248 CAGTGTGCTGCACTCAAAAGAGGACAGACAAAGTGTCTCTCTCTTCCAAATAC 1307
 QY 1203 GTCAACAGTGTGTGAGATGTATCTGTGCAAGAGCGAGGCAAGTCCAGTGAAGACTCT 1262
 DB 1308 GTCAACAGTGTGTGAGATGTATCTGTGCAAGAGCGAGGCAAGTCCAGTGAAGACTCT 1367
 QY 1263 CAAGACTCTTCCCTCTGCTTTAACCCTTTTGTGAGTGTATGAAGCCAGATTCAT 1322

Db	1368	CAGA-CTCTCCCCCTTGCTTAACTTTCTGACAGTATCTAAGACGCAATTCAT	1426
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Db	1427	CTGCACAAATACGTGGTGGTCTACTTTAGAGATTTGATACAAAGACATTTACAATGCT	1486
Qy	1383	CTCAGTGTCTGCCCCAAGTACACTTCATATAAGATGCCACGTCTTCTGTACCAACTT	1442
Db	1487	CTCAGTGTCTGCCCCAAGTACACTTCATATAAGATGCCACGTCTTCTGTACCAACTT	1546
Qy	1443	CTCCATGTCAAGCAGCAGGTGTCAAGCAGAGAAAAGATCACAAGCCCTGCACGATGGCTGC	1502
Db	1547	CTCCATGTCAAGTACAGGTGTGTCAAGCAGAGAAAAGATCACAAGCCCTGCACGATGGCTGC	1606
Qy	1503	TGCTCTCTTGAGCCACCACCCATAGAGACAAAGACCTTAAAGGCTTCTATCCCAACT	1552
Db	1607	TGCTCTCTTGAGCCACCACCCATAGAGACAAAGACCTTAAAGGCTTCTATCCCAACT	1666
Qy	1553	TACAGGGAAAAAACGTGTGATGATCCTCGAAGCTTACTATGACGCTTACAAACAGCCTTAG	1622
Db	1667	TACAGGGAAAAAACGTGTGATGATCCTCGAAGCTTACTATGACGCTTACAAACAGCCTTAG	1726
Qy	1623	TAAATTAACACATTTTATACCAATAATTAATTTTCAATATTTACTAATATGTGACTTAC	1682
Db	1727	TAAATTAACACATTTTATACCAATAATTAATTTTCAATATTTACTAATATGTGACTTAC	1786
Qy	1683	TAAAGATTGGAACCTACATTTTACCACTTCAAACTGTTTATATACATAGAAATCAATTACA	1742
Db	1787	TAAAGATTGGAACCTACATTTTACCACTTCAAACTGTTTATATACATAGAAATCAATTACA	1846
Qy	1743	GCTTTAATTGAAAACCTGTAACTATTTTGATTAATGCAACATAAAGCATCTTCCAAAAAA	1802
Db	1847	GCTTTAATTGAAAACCTGTAACTATTTTGATTAATGCAACATAAAGCATCTTCCAAAAAA	1906
Qy	1803	AAAAAAAAAAAAA 1814	
Db	1907	AAAAAAAAAAAAA 1918	

XX	RESULT 9
XX	AA05761
XX	ID AA05761 standard; cDNA, 1816 BP.
XX	AA05761;
XX	22-JAN-2001 (first entry)
XX	cDNA encoding a human interleukin 17 receptor-like polypeptide.
XX	Human; interleukin 17-receptor-like protein; IL17RP; osteoporosis;
KW	cellular activation; haemostasis; angiogenesis; tumour metastasis;
KW	cellular migration; ovulation; neurogenesis; arthritis;
KW	autoimmune disorder; systemic lupus erythromatosus; ss.
XX	
OS	Homo sapiens.
XX	
XX	Key
FT	Location/Qualifiers
FT	CDS 10..1290
FT	/*tag= a
FT	/product= "interleukin 17-receptor-like protein"
FT	10..66
FT	/*tag= b
FT	67..1287
FT	mat_peptide
FT	/*tag= c
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XX	W0200055204-A1.
XX	
XX	21-SEP-2000.
XX	
XX	06-MAR-2000; 2000WO-US05759.
XX	
XX	16-MAR-1999; 99US-0268311.
XX	

PA	(HMDA-) HUMAN GENOME SCI INC.
XX	
PI	Shi Y, Ruben SM;
XX	
DR	WPI; 2000-647065/62.
DR	P-Psdb; AAB18750.
XX	
PT	Novel gene encoding a polypeptide of the interleukin-17 receptor family, and an antagonist and agonist of the polypeptide, useful for treating, diagnosing, detecting and/or preventing immune system related disorders -
PS	Claim 2; Fig 1A-C; 247pp; English.
CC	The present sequence encodes a human interleukin 17-receptor-like protein (IL17RLP). The IL17RLP polypeptide is useful for screening for CC
CC	agonists and antagonists. These antagonists and agonists are useful for CC
CC	treating, diagnosing, detecting and/or preventing disorders related to CC
CC	cellular activation, hemostasis, angiogenesis, tumour metastasis, CC
CC	cellular migration, ovulation or neurogenesis, such as osteoporosis, CC
CC	arthritis and autoimmune disorders e.g. systemic lupus erythematosus.
SQ	Sequence 1816 BP; 532 A; 439 C; 399 G; 445 T; 1 other;
Query Match	97.2%; Score 1775.2; DB 21; Length 1816;
Best Local Similarity	99.1%; Pred. No. 0;
Matches 1795; Conservative 1; Mismatches 14; Indels 2; Gaps 1	
OY	3 GCGAGTGCCTGCTGTATGAACCTGGCCGCCGTGTGACAGGAGCCGTCACCCGAGAG 62
DB	7 GCGAGTGCCTGCTGTCTCTAAGCCTGGCCGCCGTGTGACAGGAGCCGTCACCCGAGAG 66
OY	63 CGACCGTTCAATGTGCTCTGAAACTGGGCCATCTCCAGAGTGATGCTACAATGAT 122
DB	67 CGACCGTTCAATGTGCTCTGAAACTGGGCCATCTCCAGAGTGATGCTACAATGAT 126
OY	123 CTATATCCCCGAGACTTAGGGACCTCCGAGTAGAACCTGTTCACACTAGTGTTCACACA 182
DB	127 CTAAATCCCAGAGACTTAGGGACCTCCGAGTAGAACCTGTTCACACTAGTGTTCACACA 186
OY	183 GGGGACTATTCAATTTTATGATGATGTAAGCTGGGACTCCGGGCGAGATGCCAGCATCCGC 242
DB	187 GGGGACTATTCAATTTTATGATGATGTAAGCTGGGACTCCGGGCGAGATGCCAGCATCCGC 246
OY	243 TTGTGAAGGGCCACCAGAATTTGTGTGACGGGCAAAAACAATTCAGTCTCACAGCTGT 302
DB	247 TTGTGAAGGGCCACCAGAATTTGTGTGACGGGCAAAAACAATTCAGTCTCACAGCTGT 306
OY	303 GTGAGTGCAATTACACAGAGGCTTCCAGACTCAGACCAAGACCTCTGTGTGTAAATGG 362
DB	307 GTGAGTGCAATTACACAGAGGCTTCCAGACTCAGACCAAGACCTCTGTGTGTAAATGG 366
OY	363 ACATTTTCCCTATTCGAGTTCCTCCGTAGAGCTGAACAAGTCTATTTATATGGGGCCAT 422
DB	367 ACATTTTCCCTATTCGAGTTCCTCCGTAGAGCTGAACAAGTCTATTTATATGGGGCCAT 426
OY	423 AATATTTCTAATGCAAAATGATGAATGAATGATGAGCCCTTCATGTCTGTAAATTTCACTCA 482
DB	427 AATATTTCTAATGCAAAATGATGAATGAATGATGAGCCCTTCATGTCTGTAAATTTCACTCA 486
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DB	487 CGAGGCTGCCTAGACCAATATAATGATAAAAAAAAGTGTGTCAGAGCCGGAGGCTG 546
OY	543 TGGGATCCGAACATCACTGCTTTGTAGAAAGATGAGAGACATGAGAGTGAATTTCACA 602
DB	547 TGGGATCCGAACATCACTGCTTTGTAGAAAGATGAGAGACATGAGAGTGAATTTCACA 606
OY	603 ACCGACTCCCGGGGAAAACAGATACATGGCTCTTATCCAAACAGACATATATCGGGTTT 662
DB	607 ACCGACTCCCGGGGAAAACAGATACATGGCTCTTATCCAAACAGACATATATCGGGTTT 666
OY	663 TCTAGGAGTTTGAGCCACACAGAAAGAAACAAACGACAGCTTCAGTGTGATTCAGTG 722

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Db 667 TCTCAGGTGTTTACGACACCCAGAAAGAAACAAACCGAGCTTCAGTGGATTCACAGTG 726
Qy 723 ACTGGGATATAGTAAGGTGTACGTGACGTACCTCATATTTCTCTACTTGTGGACG 782
Db 727 ACTGGGATATAGTAAGGTGTACGTGACGTACCTCATATTTCTCTACTTGTGGACG 786
Qy 783 GACTGCATCCGACATTAAGGAACAGTTGTGCTGTGCCCAACAAACAGGCGTCCCTTCCT 842
Db 787 GACTGCATCCGACATTAAGGAACAGTTGTGCTGTGCCCAACAAACAGGCGTCCCTTCCT 846
Qy 843 CTGGATTAACAACAAAGCAAGCCGGAGGTGGCTGCTCTCTCTCTGCTGTCTGTGCTG 902
Db 847 CTGGATTAACAACAAAGCAAGCCGGAGGTGGCTGCTCTCTCTCTGCTGTCTGTGCTG 906
Qy 903 GTGGCCACATGGGTGTGGGTGGGAGGATCTATCTAATGTGGAGGACGAAAGATCAAG 962
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Qy 963 AAGACTTCTTTTCTACACACACACTACTGCCCCCATTAAGGTTCTGTGTTTACCA 1022
Db 967 AAGACTTCTTTTCTACACACACACTACTGCCCCCATTAAGGTTCTGTGTTTACCA 1026
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Db 1027 TCTGAAATATGTTTCCATCAACAAATTTGTTACTTCACTGAATTTCTTCAAAACATTC 1086
Qy 1083 AAGAGGAGGTCTCTCTTGAAGGCAAGAAAGAAAGAAAGAAAGAAAGAAAGTGGTCCAGTG 1142
Db 1087 AAGAGGAGGTCTCTCTTGAAGGCAAGAAAGAAAGAAAGAAAGAAAGTGGTCCAGTG 1146
Qy 1143 CAGTGGCTTCCACTCAACAAAGAGGACGACAAAGTGTCTTCTCTTCTTCTTCAATGAC 1202
Db 1147 CAGTGGCTTCCACTCAACAAAGAGGACGACAAAGTGTCTTCTCTTCTTCTTCAATGAC 1206
Qy 1203 GTCAACAGTGTGTGCATGTGTACCTGTGGACAGAGGAGGAGTCCAGTGAATCTCT 1262
Db 1207 GTCAACAGTGTGTGCATGTGTACCTGTGGACAGAGGAGGAGTCCAGTGAATCTCT 1266
Qy 1263 CAAGACCTCTCCCTGCTTGAAGGCAAGTGTGTGAGGATGTAGAGGCCAGATTCAT 1322
Db 1267 CAAGAC-TCCTCCCTGCTTGAAGGCAAGTGTGTGAGGATGTAGAGGCCAGATTCAT 1324
Qy 1323 CTGCACAAATAGCTGTGTGTCTTCTTGAAGATGTATACAAAGACATTAACATGCT 1382
Db 1325 CTGCACAAATAGCTGTGTGTCTTCTTGAAGATGTATACAAAGACATTAACATGCT 1384
Qy 1383 CTGAGTGTCTGCCCAAGTACCACTTCATGAAGATGCCATGCTTCTGTGCAAACTT 1442
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Qy 1683 TAAAGATGAGAACTACATTTTCAACTTCAAGCTGTTTATATACATAGAAATCAATTA 1742
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Db 1745 GTTTAATGAAAGAACTATTAACCATTTTGTATTAATGCAACAATAAAGCATCTTACCCAAA 1804
Qy 1803 AAAAAAAAAA 1814
Db 1805 AAAAAAAAAA 1816

RESULT 10
AAZ52035
ID AAZ52035 standard; cDNA; 1816 BP.
XX
XX AAZ52035;
XX
XX 09-AUG-2000 (first entry)
XX
XX
XX CDNA encoding interleukin 17-like receptor protein (IL17RLP)-1.
XX
XX Interleukin-17-like receptor protein; IL-17RLP; cytokine receptor;
XX resistant chronic infection; acute infection; mycobacterial infection;
XX T-cell proliferation; IL-2 biosynthesis; lymphocytic leukaemia;
XX T-cell mediated autoimmune disease; hematopoiesis; sepsis; hybridoma;
XX IL-6 expression; myeloma; plasmacytoma; Lemert's lymphoma;
XX Immunoprotective; cytostatic; hematopoietic; proliferative;
XX antibacterial; ss.
XX
XX Homo sapiens.
XX
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XX Key Location/Qualifiers
XX CDS 10..1290
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XX mat_peptide 52..1287
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XX
XX WO200015759-A1.
XX
XX 23-MAR-2000.
XX
XX 15-SEP-1999; 99WO-US21048.
XX
XX 16-SEP-1998; 98US-0154219.
XX 16-SEP-1998; 98MO-US19121.
XX 16-MAR-1999; 99US-0268311.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Shi Y;
XX
XX MPI, 2000-271403/23.
XX
XX P-PSDB; AAY70591.
XX
XX Novel polynucleotides encoding interleukin-17-like receptor protein,
XX useful for diagnosis and treatment of immune system-related disorders,
XX e.g. sepsis and cancers -
XX
XX Claim 2; Fig 1; 147bp; English.
XX
XX The patent relates to novel interleukin-17-like receptor
XX protein (IL-17RLP). IL-17RLP is a homologue of the IL-17 receptor and has

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CC a wide range of cytokine receptor-like activities. IL-17Rlp or its
CC agonists may be used to enhance host defenses against resistant chronic
CC and acute infections, e.g., mycobacterial infections, via the attraction
CC and activation of microbicidal leukocytes. It may also be used to
CC increase T-cell proliferation by stimulating IL-2 biosynthesis, for the
CC treatment of T-cell mediated autoimmune diseases and lymphocytic
CC leukemias. IL-17Rlp may also be used to regulate hematopoiesis and to
CC treat sepsis. Extracellular IL-17Rlp domains may be used as antagonists
CC of IL-17Rlp. IL-17Rlp agonists and antagonists can also be used to
CC modulate IL-6 expression, useful in treatment of cancers such as
CC myelomas, plasmacytomas and hybridomas and Lennert's lymphoma. The
CC present cDNA sequence encodes human IL-17Rlp. This cDNA sequence was
CC discovered in a cDNA library derived from human adult pulmonary tissue.
CC
XX
Sequence 1816 BP; 532 A; 439 C; 399 G; 445 T; 1 other;

Query Match 97.2%; Score 1775.2; DB 21; Length 1816;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1795; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

QY 3 GCGATGCTCGCTGCTGATAGCGCTGCGCGCTGTCAGAGCCGCTACCCCGAGAG 62
DB 7 GCGATGCTCGCTGCTGCTGATAGCGCTGCGCGCTGTCAGAGCCGCTACCCCGAGAG 66
QY 63 CCGACGCTCAATGTCGCTGTAATCGGCGCATCTCCAGATGATGATCAATGAT 122
DB 67 CCGACGCTCAATGTCGCTGTAATCGGCGCATCTCCAGATGATGATCAATGAT 126
QY 123 CTATATCCCGGAGACTGAGGAGCCTCGAGTGAACCTGTTCACTAGTGTGACACA 182
DB 127 CTATATCCCGGAGACTGAGGAGCCTCGAGTGAACCTGTTCACTAGTGTGACACA 186
QY 183 GGGGACTATTCATTTTGTATGATGATGATGATGATGATGATGATGATGATGAT 242
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DB 487 CCGAGGCTGCTAGCCCATATGATGATGATGATGATGATGATGATGATGATGATGAT 546
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DB 547 TGGGATCCGAAATCACTGCTTGTAGAGAGATGAGAGAGCAGTAGAAGTGAATCTTACA 606
QY 603 ACCATCTCCCTGGGAAAACAGATACATGCTTATTCACACAGCACTATCATCGGCTTT 662
DB 607 ACCATCTCCCTGGGAAAACAGATACATGCTTATTCACACAGCACTATCATCGGCTTT 666
QY 663 TCCAGGTGTTAGCCACACGAGAAACAAACGAGCTTCAGTGGATTTTCAAGT 722
DB 667 TCCAGGTGTTAGCCACACGAGAAACAAACGAGCTTCAGTGGATTTTCAAGT 726
QY 723 ACTGGGATAGTAAAGGTGTACGCTGACAGTCAATATTTTCTTACTTGTGGAGC 782
DB 727 ACTGGGATAGTAAAGGTGTACGCTGACAGTCAATATTTTCTTACTTGTGGAGC 786
QY 783 GACTGATCGACATTAAGAAACAGTTGTGCTGCTGCCACAAAGGCGTCCCTTCCCT 842

DB 787 GACTGATCGACATTAAGAAACAGTTGTGCTGCTGCCACAAACAGCGCTCCCTTCCCT 846
QY 843 CTGATTAACAAACAAAGCAAGCCGGAGGCTGAGCTCTCTCTCTGCTGCTGCTGCTG 902
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QY 903 GTGGCCACATGGGT 962
DB 907 GTGGCCACATGGGT 966
QY 963 AAGACTTCTTTTCTTCAACACACATCTGCCCCCATTTAAGTTTGTGTGTGTGTGTGT 1022
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DB 1087 AGAAGTGAAGTCACTCTTGAAGAGGCAAGAAAGAAATGACAGATGGGTCCAGTG 1146
QY 1143 CAGTGGCTTCCCACTTAAAGAGGACAGACAAAGTGTCTTCTTCTTCTTCAATGAC 1202
DB 1147 CAGTGGCTTCCCACTTAAAGAGGACAGACAAAGTGTCTTCTTCTTCTTCAATGAC 1206
QY 1203 GTCAACAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1262
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QY 1263 CAAGACTTCTTCCCTGCTTTTAACTTTTCTGAGTATGATGATGATGATGATGAT 1322
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DB 1325 CTGCACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1384
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DB 1385 CTCAGTGTCTGCCCCCAAGTACCTTCAATGATGATGATGATGATGATGATGATGAT 1444
QY 1443 CTCATGTCAAGCAGAGGTGTCAAGAGGAAAGATCAAGAGCTGCGCAGATGCTGC 1502
DB 1445 CTCATGTCAAGCAGAGGTGTCAAGAGGAAAGATCAAGAGCTGCGCAGATGCTGC 1504
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DB 1505 TGTCTCTTGTAGCCCACTGATGAGAGCAAGAGCTTAAAGCTTCTTCTTCTTCAAT 1564
QY 1563 TACAGGAAAGAAACGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1622
DB 1565 TACAGGAAAGAAACGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1624
QY 1623 TAATTAACATTTTATACCAATTAATTTTCAATATTTTCAATATGATGATTAAC 1682
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QY 1743 GCTTTAATGAAACATTTTCAACTTCAAGCTGTTTAACTTAAAGTAAATCAATTTTCA 1802
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DB 1805 AAAAAAAAAAAAAA 1816

RESULT 11

AA235746
ID AA235746 standard; cDNA; 1816 BP.
AC AA235746;
XX
DT 01-FEB-2000 (first entry)
XX
DE Human interleukin 17 receptor like protein encoding cDNA.
XX
KW Human; interleukin 17 receptor like protein; IL17RP; IL-17;
XX diagnosis; detection; immune system related disorder; haemostasis;
KW cellular activation; angiogenesis; tumour metastasis; ovulation;
KW cellular migration; neurogenesis; infection; T-cell proliferation;
KW autoimmune disease; lymphocytic leukaemia; haematopoiesis; regulation;
KW sepsis; tumour; cancer; interstitial lung disease; arthritis;
KW lymphoma; immunosuppression; immunity; inflammatory bowel disease;
KW myelo suppression; SR.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT /product= "interleukin 17 receptor like protein"
FT sig_peptide 10..66
FT /tag= b
FT mat_peptide 67..1287
FT /tag= c
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PN MO9914240-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-US19121.
XX
PR 17-SEP-1997; 97US-0059133.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Shl Y, Ruben SM;
XX
DR WPI: 2000-061918/05.
XX
DR P-PSDB; AAY49946.
XX
PT New human interleukin-17 receptor like protein, e.g. to treat disorders
XX relating to cellular activation -
XX
PS Claim 2; Fig 1; 133pp; English.
XX
CC The present sequence encodes human interleukin 17 receptor like protein
CC (IL17RP), isolated from a cDNA library of human adult pulmonary tissue.
CC IL17RP and its agonists can be used to treat disorders relating to
CC cellular activation, haemostasis, angiogenesis, tumour metastasis,
CC cellular migration and ovulation, and neurogenesis. They can also be
CC used to enhance host defences against resistant chronic and acute
CC infections, e.g. mycobacterial infections via the attraction and
CC activation of microbial leukocytes. IL17RP may also be used to increase
CC T-cell proliferation by the stimulation of IL-2 biosynthesis for the
CC treatment of T-cell mediated autoimmune diseases and lymphocytic
CC leukaemias, to regulate haematopoiesis by regulating the activation and
CC differentiation of various haematopoietic progenitor cells, e.g. to
CC release mature leukocytes from the bone marrow following chemotherapy,
CC i.e. in stem cell mobilisation or to treat sepsis. The products can also
CC be used for the diagnosis or treatment of immune system related disorders
CC e.g. tumours, cancers, interstitial lung disease, and any dysregulation
CC of immune cell function including autoimmunity, arthritis, leukaemias,
CC lymphomas, immunosuppression, immunity, humoral immunity, inflammatory
CC bowel disease, or myelo suppression.
XX
SQ Sequence 1816 BP; 532 A; 439 C; 399 G; 445 T; 1 other;

Matches 1795; Conservative 1; Mismatches 14; Indels 2; Gaps 1;
QY 3 GCGATGTCGCTGCTGTAATAGCCTGCGCGCTGTGAGAGCCGCCATCCGAGAG 62
DB 7 GCGATGTCGCTGCTGCTGTAATAGCCTGCGCGCTGTGAGAGCCGCCATCCGAGAG 66
QY 63 CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGAATGCTTACAACATGAT 122
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DB 127 CTAATCCCGGAGCTTGAGGGGACCTCCGAGTAAGAACCTGTTACAACATGATGGAACA 186
QY 183 GGGGACTATTCATTTGATGATGTAATGAGTGGGTAAGTCCGGGAGATCCGATCCGC 242
DB 187 GGGGACTATTCATTTGATGATGTAATGAGTGGGTAAGTCCGGGAGATCCGATCCGC 246
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DB 247 TTGTTGAAGCCACCAAGATTTGTGTGACGGGCAAAAGCACTTCAGTCTCAAGCTGT 306
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DB 367 ACATTTTCCATATGCGCTCCCTGTAGAGCTGAACACAGTCTATTTCAATGGGGCCAT 426
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DB 427 AATATTTCCATATGCAATATGTAATGTAAGATGAGCCCTTCATGCTGTGTAATTCACCTCA 486
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DB 487 CCAAGCTGCTTAGACCAATATGAAATATTAATAAATAAGTGTCAAGGCCGGAAGCCTG 546
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DB 547 TGGGATCCGAACATCACTGCTGTGTAAGAAATGAGAGACAGTGAAGTGAATTCACCA 606
QY 603 ACCACTCCCTGGGAAACAGATATACATGAGCTCTTATCCAACACAGCACTATCATCGGGTT 662
DB 607 ACCACTCCCTGGGAAACAGATATACATGAGCTCTTATCCAACACAGCACTATCATCGGGTT 666
QY 663 TCTCAGTGTGTTGAGCCACACACCAAGAAACAAACGCGAGCTTCAGTGTATTCAGTG 722
DB 667 TCTCAGTGTGTTGAGCCACACCAAGAAACAAACGCGAGCTTCAGTGTATTCAGTG 726
QY 723 ACTGGGATGAGAGGTGCTACGGGTGAGCTGATCCATATTTCTACTTGTGGCAGC 782
DB 727 ACTGGGATGAGAGGTGCTACGGGTGAGCTGATCCATATTTCTACTTGTGGCAGC 786
QY 783 GACTGCATCCGACATATTAAGAAACAGTGTGCTGCTCCCAAAACAGGGGTCCTTTCCCT 842
DB 787 GACTGCATCCGACATATTAAGAAACAGTGTGCTGCTCCCAAAACAGGGGTCCTTTCCCT 846
QY 843 CTGATTAACAACAAAGAGAGCGGGAGGCTGCTCTCTCTCTGCTGTCTGCTG 902
DB 847 CTGATTAACAACAAAGAGAGCGGGAGGCTGCTCTCTCTCTGCTGTCTGCTG 906
QY 903 GTGGCACAATGGGTGCTGTGGGAGGAGTATCTTAATGTGAGGACGAAGAAGTCAAG 962
DB 907 GTGGCACAATGGGTGCTGTGGGAGGAGTATCTTAATGTGAGGACGAAGAAGTCAAG 966
QY 963 AAGACTTCCTTTTACACCACTACTGCCCCCATTAAGTGTCTGTGTTACCA 1022
DB 967 AAGACTTCCTTTTACACCACTACTGCCCCCATTAAGTGTCTGTGTTACCA 1026
QY 1023 TCTGAATATGTTTTCATCAACAATTTGTTACTTCAATTTCTTCAAAACCATTCG 1082
DB 1027 TCTGAATATGTTTTCATCAACAATTTGTTACTTCAATTTCTTCAAAACCATTCG 1086

Query Match 97.2%; Score 1775.2; DB 21; Length 1816;
Best Local Similarity 99.1%; Pred. No. 0;

[illegible]

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Dd	1365	GGCTTGCCACTCAAAGAAGCAGACAAAGTCGTCTTCTCTTTCCAATGACGTCA	1424
Qy	1207	ACAAGTGTGGAGTGTACTCTGTGGCAAGCAGAGGCAGTCCAGTAGAACCTTCAG	1286
Dd	1425	ACAGTGTGGAGTGTACTCTGTGGCAAGCAGAGGCAGTCCAGTAGAACCTTCAG	1484
Qy	1267	ACCTGTCCCCCTTGAACCTTTCTGACATGATCTTAAGAAAGCAGATTACATGCG	1326
Dd	1485	ACCTGTCCCCCTTGAACCTTTCTGACATGATCTTAAGAAAGCAGATTACATGCG	1544
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Dd	1665	ATGTCAACGACAGGTGTGACACAGAAAAATAACAAGCCTGCAAGATGCGTGTCT	1724
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Dd	1725	CCTTGTAGCCCAACCAGTAGAAGCAAGACCTTAAGAGCTTCTATCCACCAATTACA	1784
Qy	1567	GGGAAAAACGTGTGATGATCTTGAAGCTTACTATGACGCTTACAAACAGCTTGAAT	1626
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Qy	1627	TAAACATTTTATACCAATAAAATTTTCAATATTTACTAATATGATGATTAACCTAAC	1686
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XX	DT	11-FEB-2002 (first entry)	
DE	XX	Human IL-17 receptor like protein #2 coding sequence.	
XX	XX		
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KM	antiproliferative; antimicrobial; anorectic; neurotrophic; neuroprotective;		
KM	antiasthmatic; antiallergic; dermatological; cytostatic; gene therapy;		
KM	interleukin 17; immune system disorder; infection; weight; reproductive;		
KM	neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation;		
KM	glomerulonephritis; bone; osteoporosis; vascular system; ischemia; eye;		
XX	tumour; S6.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
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CD	FT	/**tag= a	
FT	FT	/product= "Human IL-17 receptor-like protein #2"	
XX	XX		


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Db 1089 ACCTCAACAAGTGTGAGTGTACTCTGTGCAAGAGCGAGGAGTCCAGTGAAGACT 1148
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Db 1149 CTCAGAAGCTCTTCCCTTCCCTTAACTTTTCTGAGTGTCTAAGAACCAAGATTC 1208
Qy 1321 ATCTGACAAATACGTGAGTGTCTACTTGAAGATTTGATTAACAAAAGAGATTAACAATG 1380
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Qy 1441 TTCTCAATGTCAGACAGCAGGTGTCAAGAGAAAAAAGATCAACAAGCTGCGACGATGGCT 1500
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Qy 1501 GCTGCTCTTGTAGCCCACTGAGAGAGAGAAAGCTTAAAGGCTCTTATCCACCA 1560
Db 1389 GCTGCTCTTGTAGCCCACTGAGAGAGAGAAAGCTTAAAGGCTCTTATCCACCA 1448
Qy 1561 ATTACAGGAAAAAAGCTGTGATGATCTGAAGCTTACTATGAGCCTTACAACAGCCTT 1620
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Qy 1681 ACTAAGATTTGAGAACTACATTTTACAACTTCAAGCTGTTTATACATAGAAATCAATTA 1740
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Qy 1741 CAGCTTTAATGAAAACTGTACCATTTTGTATATGACAAATTAAGACATCTTCCAAAAA 1800
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Qy 1801 AAAAAAAAAAAAAA 1813

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Db 1689 AAAAAAAAAAAAAA 1701
RESULT 15
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XX
XX AAF64039;
AC
XX
XX 05-APR-2001 (first entry)
DT
XX
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DE
XX
XX Secreted protein; prevention; treatment; diagnosis; disease;
KM
XX infection; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200100806-A2.
PN
XX
XX 04-JAN-2001.
PD
XX
XX 21-JUN-2000; 2000MO-IB00951.
PF
XX
XX 25-JUN-1999; 99US-0141032.
PR
XX 21-DEC-1999; 99US-0469099.
XX
XX (BEST ) GENSER.
PA
XX
XX Dumas Milne Edwards J, Bouquelere L, Jobert S;
PI
XX WPI; 2001-071487/08.
XX
XX
XX 49 Secreted proteins and the nucleic acids encoding them, useful in
PT gene therapy and for detecting similar sequences in samples -
XX
XX
XX Claim 1; Page 259-261; 307pp; English.
XX
XX The present invention relates to 49 Secreted proteins and the cDNAs
CC encoding them. The protein and nucleic acids may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate protein expression.
XX
XX
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Best Local Similarity 92.3%; Pred. No. 0; Mismatches 12; Indels 128; Gaps 1;
Matches 1673; Conservative 0;
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Db 248 ----- 247
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Db 248 -----T 248

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 22:37:09 ; Search time 4652.87 Seconds
(without alignments)
11427.544 Million cell updates/sec

Title: US-09-778-971-1

Perfect score: 1827

Sequence: 1 cggcgatgcctcgtgctg.....aaaaaaaaaaaaaaaaaaaaa 1827

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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11: gb_ats.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_ats.*

28: em_un.*

29: em_vi.*

30: em_hcg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

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34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1827	100.0	1828	9	AF208110	AF208110 Homo sapi
2	1786	97.8	1841	6	AX253204	AX253204 Sequence
3	1786	97.8	1841	6	AX365258	AX365258 Sequence
4	1785.6	97.7	1796	6	AX350967	AX350967 Sequence
5	1783.8	97.6	2042	9	BC000980	BC000980 Homo sapi
6	1782.8	97.6	1818	6	AX191534	AX191534 Sequence
7	1775.6	97.2	1816	9	AF212365	AF212365 Homo sapi
8	1558.2	85.3	1583	9	AF250309	AF250309 Homo sapi
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11	1527.8	83.6	1701	6	AX061651	AX061651 Sequence
12	1518.4	83.1	1713	6	AX253209	AX253209 Sequence
13	1509.2	82.6	1515	6	AX092426	AX092426 Sequence
14	1509.2	82.6	1515	6	AX180774	AX180774 Sequence
15	1509.2	82.6	1515	6	AX376332	AX376332 Sequence
16	1502.6	82.2	1509	6	AX191524	AX191524 Sequence
17	1081.6	59.2	1506	6	AX350969	AX350969 Sequence
18	1078	59.0	2856	9	AF208111	AF208111 Homo sapi
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34	64	3.5	6763	6	AX458551	AX458551 Sequence
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ALIGNMENTS

RESULT 1
AF208110

LOCUS

DEFINITION

complete cds.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1828)

REFERENCE

AUTHORS

Tian, B., Sawyer, J.R., Largaespada, D.A., Jenkins, N.A., Copeland, N.G.

and Shaughnessy, J.D. Jr.

AF208110 1828 bp mRNA linear PRI 17-JUL-2000
Homo sapiens IL-17 receptor homolog precursor (EVI27) mRNA,
complete cds.

AF208110 GI:9246432

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1828)

REFERENCE

AUTHORS

Tian, B., Sawyer, J.R., Largaespada, D.A., Jenkins, N.A., Copeland, N.G.

and Shaughnessy, J.D. Jr.


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Db 1801 AAAAAAAAAAAAAAAAAAAAAAAAAA 1827

RESULT 2
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DEFINITION Sequence 1 from Patent WO0168705.
ACCESSION AX253204
VERSION AX253204.1 GI:15986346
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (Bases 1 to 1841)
AUTHORS Jing, S., Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S. and
Nguyen, H.Q.
TITLE Il-17 receptor like molecules and uses thereof
JOURNAL Patent: WO 0168705-A 1 20-SEP-2001;
Amgen Inc. (US)
FEATURES Location/Qualifiers
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50. .1558
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/db_xref="GI:15986347"
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GCLDHI MKYKKKCVKAGSLMDPNITACKNEETVEVNTFTPLGNRYMALLOHSTIIG
FSQVFEHQKQTRASVIVPVTSSEGTATVLTFFPTCGSDCI RHKGTVLCVCTGV
PFPDNNKSPKPGWLPLLLLSLVATVWAGIYLMRHERIKKTSFSTTTLLPPIKV
LVVYPSICFHHTICYFTELQNRSEVILEKWKQKIAEMQVLTATQKKAADKV
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ORIGIN
Query Match 97.8%; Score 1786; DB 6; Length 1841;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CGCGCATGTCGTGCTGATAGCCTGGCGCGCTGTGCAGGAGCGCGGTACCCCGAG 60
Db 45 CGCGCATGTCGTGCTGCTGATAGCCTGGCGCGCTGTGCAGGAGCGCGGTACCCCGAG 104
Qy 61 AGCGGACGCTTCAATGTCGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACTG 120
Db 105 AGCGGACGCTTCAATGTCGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACTG 164
Qy 121 ATCTAATCCCGGACATTTGAGGACCTCCGAGTGAAGCTTACAACTAGTGTGCAAA 180
Db 165 ATCTAATCCCGGACATTTGAGGACCTCCGAGTGAAGCTTACAACTAGTGTGCAAA 224
Qy 181 CAGGGGACATTTCAATTTTGTATGAATGTAAGTGGTACTCCGGGCGAGATGCCAGATCC 240
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RESULT 3

AX365258
LOCUS Sequence 17 from Patent WO0208285. 1841 bp DNA linear PAT 15-FEB-2002
ACCESSION AX365258
VERSION AX365258.1 GI:18697003
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM human.
REFERENCE 1 Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S., Nguyen, H.Q. and
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
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JOURNAL Patent: WO 0208285-A 17 31-JAN-2002;
Angen, Inc. (US)
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BASE COUNT 522 a 455 c 416 g 448 t
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Best Local Similarity 99.7%; Pred. No. 0;
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DEFINITION	AX350967		
ACCESSION	AX350967.1	GI:18616343	
VERSION			
KEYWORDS	unidentified.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1		
AUTHORS	Gorman,D.M.		
TITLE	Mammalian receptor proteins; related reagents and methods		
JOURNAL	Patent: WO 0190358-A 1 29-NOV-2001;		
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RESULT 5					
BC000980					
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DEFINITION	Homo sapiens.	clone MGC:5245 IMAGE:2985728.	mRNA,	complete cds.	

REFERENCE	Mammalia, Eutheria, Plimates, Carnivora, Nonartiodactyla, nonom.
AUTHORS	1 (bases 1 to 2042)
TITLE	Strausberg, R.
JOURNAL	Direct Submission Submitted (16-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.ncbi.nih.gov

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 3 Row: n Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9246432.
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DEFINITION Homo sapiens IL-17B receptor (IL17BR) mRNA, complete cds.
ACCESSION AF212365
VERSION AF212365.1 GI:8705221
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1816)
AUTHORS Shi,Y., Ullrich,S.J., Zhang,J., Connolly,K., Grzegorzewski,K.J.,
Barber,M.C., Wang,W., Mathen,K., Hodge,V., Fisher,C.L., Olsen,H.,
Ruben,S.M., Knyazev,I., Cho,Y.H., Kao,V., Wilkinson,K.A.,
Carrell,J.A. and Ebner,R.
TITLE A novel cytokine receptor-ligand pair. Identification, molecular
characterization, and in vivo immunomodulatory activity
J. Biol. Chem. 275 (25), 19167-19176 (2000)
JOURNAL 20317118
MEDLINE 10749887
PUBMED
REFERENCE 2 (bases 1 to 1816)
AUTHORS Shi,Y.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-1999) Molecular Biology, Human Genome Sciences,
Inc., 9410 Key West Avenue, Rockville, MD 20850, USA
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RESULT 8
AF250309 1593 bp mRNA linear PRI 17-APR-2001
LOCUS Homo sapiens putative cytokine receptor CRL4 precursor mRNA,
DEFINITION complete cds.
ACCESSION AF250309
VERSION AF250309.1 GI:13649476
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1593)
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AUTHORS Zhang, W. and Cao, X.
TITLE Direct Submission
JOURNAL Submitted (29-MAR-2000) Department of Immunology, Second Military
Medical University & Shanghai Brilliance Biotechnology Institute,
800 Xiangyin Rd., Shanghai 200433, P.R. China
FEATURES
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DEFINITION	Sequence 4 from Patent WO0168705.
ACCESSION	AX253207
VERSION	AX253207.1
KEYWORDS	GI:15986348
DNA	linear
PAT	05-OCT-2001

human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2015)
 AUTHORS Jing,S., Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S. and
 Nguyen,H.Q.
 TITLE IL-17 receptor like molecules and uses thereof
 JOURNAL Patent: WO 0168705-A 4 20-SEP-2001;
 Angen Inc. (US)
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RESULT 11

AX061651 LOCUS 1701 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 56 from Patent WO0100806.
ACCESSION AX061651
VERSION AX061651.1 GI:12406761
KEYWORDS SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1701)
AUTHORS dumas mlne Edwards,J.B., Bougueleret,L. and Jobert,S.
TITLE Complementary dna's encoding proteins with signal peptides
JOURNAL Patent: WO 0100806-A 56 04-JAN-2001;
GENSET (PR)
FEATURES
source
1..1701
/organism="Homo sapiens"
/db_xref="taxon:9606"

[illegible]

GenCore version 5.1.4 p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 23:21:54 ; Search time 3965.62 Seconds
(without alignments)
11663.832 Million cell updates/sec

Title: US-09-778-971-2

Perfect score: 2856

Sequence: 1 cggcgatgctcgtcgtgctg.....aaaaaaaaaaaaaaaaaaaaa 2856

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_eston:*

17: gb_gss:*

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22: em_gss_fun:*

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25: em_gss_other:*

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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	765.4	26.8	908	9	AL565993
2	689.6	24.1	869	9	AL535617
3	638.4	22.4	652	14	BM693867
4	630.6	22.1	657	13	BM670929
5	621.6	21.8	641	10	BE539514
6	619.6	21.7	946	13	BI823321

C 7	598.2	20.9	630	12	EG4333769
8	585	20.5	680	10	AW970151
9	554.2	19.4	561	10	AW675096
C 10	497	17.4	510	10	AW299271
C 11	493	17.3	509	12	BF110326
C 12	477.4	16.7	502	10	BE466508
C 13	476.8	16.7	615	10	AV685699
C 14	475.2	16.6	484	12	BF064177
C 15	475	16.6	488	9	AA514396
C 16	474.8	16.6	491	10	AW837146
C 17	473.8	16.6	703	10	AV709899
18	462.4	16.2	773	13	BI103740
19	449.4	15.7	710	10	BB653710
C 20	438.6	15.4	457	9	AA677205
C 21	436.2	15.3	470	12	BF921554
C 22	436	15.3	477	9	AA287951
C 23	434.2	15.2	460	12	BF740045
C 24	432.2	15.1	437	9	AI032064
C 25	431.4	15.1	435	17	AQ309936
C 26	427.4	15.0	499	12	BF920093
C 27	415.2	14.5	420	9	AI401622
C 28	410.4	14.4	434	9	AI826949
C 29	409	14.3	427	9	AI627783
C 30	404.4	14.2	414	9	AI911549
C 31	404	14.1	416	10	BE047352
32	398.8	14.0	551	12	EG384365
33	396.6	13.9	588	13	BI360842
C 34	396.2	13.9	409	12	BF194822
C 35	391.8	13.7	401	9	AI538624
36	389.4	13.6	440	14	R74129
C 37	389.2	13.6	394	14	W61239
C 38	387.6	13.6	398	9	AA847767
39	387.2	13.6	646	10	BB644125
C 40	380.4	13.3	403	10	AW025192
C 41	380.2	13.3	392	9	AI913613
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44	372.6	13.0	413	14	W61238
C 45	367.4	12.9	373	9	AI672344

ALIGNMENTS

RESULT 1
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LOCUS AL565993 908 bp mRNA linear EST 16-FEB-2001
DEFINITION AL565993 LTI_FL013_FBrn1 Homo sapiens CDNA clone CS0DF016YG03 3
prime, mRNA sequence.
ACCESSION AL565993
VERSION AL565993.1 GI:12917920
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 908)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length CDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source

1. 908
/location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DF016YG03"
/clone_lib="LTI_FL013_FBrn1"
/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
/lab_host="DH10B"

modified polylinker; Site_1: EcoR I; Site_2: Not I; UF-E-DWI is a normalized cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATTAGCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

188 a	167 c	135 g	162 t
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BASE COUNT

Query Match		22.4%	Score 638.4	DB 14	Length 652
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Matches	650	Conservative	0	Mismatches	1
				Indels	1
				Gaps	1
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Qy	2050	CATCTGAATATGTTTCCATCACACAATTTGTACTTCTACGTAATTTCTTCAAAACCAT	2109		
Db	61	CATCTGAATATGTTTCCATCACACAATTTGTACTTCTACGTAATTTCTTCAAAACCAT	120		
Qy	2110	GCAGAAGTGAGGTTCATCTTTGAAAAGTGGCAGAAAAAGAAAAATAGCAGAGATGGTCCAG	2169		
Db	121	GCAGAAGTGAGGTTCATCTTTGAAAAGTGGCAGAAAAAGAAAAATAGCAGAGATGGTCCAG	180		
Qy	2170	TGAGTGGCTTTGCCATCAAAAAGAGGCGACAGACAAAGTCGTCTTCTTTCCTTTC	2229		
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Db	541	GCTGCTCTTTGTAGCCCAACCCATGAAAGCAAGAGACCTTTAAAGGCTTCTATCCCA	600		
Qy	2590	ATTACAGGG-AAAAAACGTGTGATGATCTCTGAAGCTTACTATGCAGCGCTACA	2640		
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RESULT 4	BM670929/c	657 bp	mRNA	linear	EST 27-FEB-2002
LOCUS	BM670929.1				
DEFINITION	UI-B-DWI-ahe-1-22-0-UI.s1 UI-E-DWI Homo sapiens cDNA clone				
	UI-B-DWI-ahe-1-22-0-UI 3', mRNA sequence.				
ACCESSION	BM670929				
VERSION	BM670929.1	GI:18980826			

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DEFINITION
522 bp mRNA linear EST 28-FEB-2002
UI-E-DWI-ahe-i-22-0-UI.r1 UI-E-DWI Homo sapiens cDNA clone
UI-E-DWI-ahe-i-22-0-UI 5', mRNA sequence.
ACCESSION
BM693867
VERSION
BM693867.1
KEYWORDS
GI:19007125
SOURCE
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ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Bonaldo M.F., Lennon G. and Soares M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
9704477
COMMENT
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
FEATURES
Location/Qualifiers
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/tissue_type="lens"
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/notes="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a"

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 Matches 635; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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 DB 1 ACTCAAAAGAGGCGACGACAAAGTCGCTCTCTTCCCAATGACGTCACACGTGTG 60

QY 2244 TCGATGTGACCTGTGGCAAGCGAGGCGAGTCCAGTGAAGTCTCTCAAGACCTCTTC 2303
 DB 61 TCGATGTGACCTGTGGCAAGCGAGGCGAGTCCAGTGAAGTCTCTCAAGACCTCTTC 120

QY 2304 CCCCTTGCCTTTAACTTTTCTGCACTGATCTAAGAGCGAGTTCATCTGCAAAATAC 2363
 DB 121 CCCCTTGCCTTTAACTTTTCTGCACTGATCTAAGAGCGAGTTCATCTGCAAAATAC 180

QY 2364 GTGGTGGTCTACTTTAGAGAGTTGATCAAAAGAGAGTTACAACTCTCTCAGTGCTGC 2423
 DB 181 GTGGTGGTCTACTTTAGAGAGTTGATCAAAAGAGAGTTACAACTCTCTCAGTGCTGC 240

QY 2424 CCCAAGTACCACTTCATGAAGGATGCCACTGCTTCTGTGCAGAACTTCTCCATGTCAAG 2483
 DB 241 CCCAAGTACCACTTCATGAAGGATGCCACTGCTTCTGTGCAGAACTTCTCCATGTCAAG 300

QY 2484 CAGCAGGTGTACGACGAGAAAGATCACAAGCTGCGACAGTGGCTGTCTCTCTGTAG 2543
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QY 2544 CCCACCCATGAGAGCAAGAGACCTTAAAGGCTTCTATCCCACTTACAGGGGAAAA 2603
 DB 361 CCCACCCATGAGAGCAAGAGACCTTAAAGGCTTCTATCCCACTTACAGGGGAAAA 420

QY 2604 AGCTGTGATGATCCTGAAGCTTACTATGAGCGCTACAAACAGCTTGTAAATTAACAT 2663
 DB 421 AGCTGTGATGATCCTGAAGCTTACTATGAGCGCTACAAACAGCTTGTAAATTAACAT 480

QY 2664 TTTATACCAATAAAATTTTCAAATATTACTAATAATGATAGCAATTAACGATTTGAA 2723
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QY 2784 AACTGTAAACATTTTGAATGATCAATCAAAATAAGCATCTTC 2823
 DB 600 AACTGTAAACATTTTGAATGATCAATCAAAATAAGCATCTTC 639

RESULT 6
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 DEFINITION 603041231F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182255 5',
 mRNA sequence.
 ACCESSION BI823321
 VERSION BI823321.1 GI:15934871
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 946)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11454 row: m column: 08
 High quality sequence stop: 795.

FEATURES

Location/Qualifiers
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 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector: pCMV-SORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library."
 BASE COUNT 240 a 239 c 243 g 224 t
 ORIGIN

Query Match 21.7%; Score 619.6; DB 13; Length 946;
 Best Local Similarity 92.9%; Pred. No. 4.4e-103;
 Matches 702; Conservative 0; Mismatches 4; Indels 50; Gaps 3;

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QY 62 GCGACCGCTTCAATGTGGCTCTGAAACTGGGCACTCTCCAGAGTGGATGCTACAACATGA 121
 DB 61 GCGACCGCTTCAATGTGGCTCTGAAACTGGGCACTCTCCAGAGTGGATGCTACAACATGA 120

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 DB 361 GACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCAATGGGCGCA 420

QY 422 TAATATTCCTAATCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTTCACTC 481
 DB 421 TAATATTCCTAATCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTTCACTC 480

QY 482 ACCAGGCTSCCTAGACCACATAATGAAATATATAAAAAGATGTGTCAAGGCCGCGAGCT 541
 DB 481 ACCA-----GGAAGCCT 492

QY 542 GTGGATCCGAACATCACTGCTTTGTAAG-AAGAAATGAGGAGACAGTAGAAGTGAATTC 600
 DB 493 GTGGATCCGAACATCACTGCTTTGTAAGAAAGATGAGGAGACAGTAGAAGTGAATTC 552

QY 601 CAACCACTCCCTGGGAAACAGATACATGGCTTCTTATCCAAACACAGCACTATATCGGGT 660
 DB 553 CAACCACTCCCTGGGAAACAGATACATGGCTTCTTATCCAAACACAGCACTATATCGGG- 611

QY 661 TTTCTCAGGTGTTGAGCCACACAGGAGAAACAAACGCGAGCTTTCAGTGTGTATTCAG 720


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Db 612 TTTCTCAGGTGTTTGAGCCACACAGAGAAACAAACGCGAGCTTCAGTGGTGAATCCAG 671
Qy 721 TGACTGGGATAGTGAAGTGGCTACGGTGCAGGTAA 756
Db 672 TGACTGGGATAGTGAAGTGGCTACGGTGCAGCTGA 707

RESULT 7
BG433769/c
LOCUS BG433769 630 bp mRNA linear EST 14-MAR-2001
DEFINITION 602497744F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4611491 5',
mRNA sequence.
ACCESSION BG433769
VERSION BG433769.1 GI:13340275
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 630)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1358 row: g column: 12
High quality sequence stop: 610.
Location/Qualifiers
1. .630
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4611491"
/clone_lib="NIH_MGC_75"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGAGCGGCCGACATG-dt(30)EN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
BASE COUNT 170 a 111 c 149 g 200 t
ORIGIN
Query Match 20.9%; Score 598.2; DB 12; Length 630;
Best Local Similarity 97.9%; Pred. No. 4e-99;
Matches 606; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 2214 TTCCTTTCTTCCAAATGCTCAACAGTGTGTGGATGGTGTGGCGAAGAGCGAGGCG 2273
Db 626 TCCTTCTTTTCCAAATGCTCAACAGTGTGTGGATGGTGTGGCGAAGAGCGAGGCG 567
Qy 2274 AGTCCAGTGAAGACTCTCAAGACCTCTTCCCTTGCCTTTAACTTTCTGCGAGTGT 2333
Db 566 AGTCCAGTGAAGACTCTCAAGACCTCTTCCCTTGCCTTTAACTTTCTGCGAGTGT 507
Qy 2334 CTAAGAAGCCAGATTTCATCTGCACAATACGTGGTGGTGTCTACTTTAGAGAGATTGATACA 2393
Db 506 CTAAGAAGCCAGATTTCATCTGCACAATACGTGGTGGTGTCTACTTTAGAGAGATTGATACA 447
Qy 2394 AAAGAGATTACATGCTCTCAGTGTCTGCCCAAGTACACCTTCATGAGGATGCCACT 2453

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Db 446 AAAGAGATTACATGCTCTCAGTGTCTGCCCAAGTACCACCTCATGAAGATGCCACT 387
Qy 2454 GCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAAGAGGAAAAAGATCACAA 2513
Db 386 GCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAAGAGGAAAAAGATCACAA 327
Qy 2514 GCCTGCCAGATGGTGTGCTCTCTTGTAGCCACCCATGAGAAGCAAGAGACCTTTAAAG 2573
Db 326 GCCTGCCAGATGGTGTGCTCTCTTGTAGCCACCCATGAGAAGCAAGAGACCTTTAAAG 267
Qy 2574 GCTTCTTATCCCACTTACAGGGAAGAAACGCTGTGATGATCCTGAGCTTACTATGCA 2633
Db 266 GCTTCTTATCCCACTTACAGGGAAGAAACGCTGTGATGATCCTGAGCTTACTATGCA 207
Qy 2634 GCCTCAAAACAGCCTTAGTAATTAATAAATTTATACCAATAAATTTTCAATATTACT 2693
Db 206 GCCTCAAAACAGCCTTAGTAATTAATAAATTTATACCAATAAATTTTCAATATTACT 147
Qy 2694 AACTAATGTAGCATTAACCTAACGATTGGAACTACATTTTACAACTTCAAAGCTGTTTTAT 2753
Db 146 AACTAATGTAGCATTAACCTAACGATTGGAACTACATTTTACAACTTCAAAGCTGTTTTAT 87
Qy 2754 ACATAGAATCAATTAACAGCTTTAATTTGAAGAACTGTAACTTTTGAATGCAACAATA 2813
Db 86 ACATAGAATCAATTAACAGCTTTAATTTGAAGAACTGTAACTTTTGAATGCAACAATA 27
Qy 2814 AAGCATCTTCCAAAAAATA 2832
Db 26 AAGCATCTTCCAAAAAATA 8

RESULT 8
LOCUS AW970151 680 bp mRNA linear EST 01-JUN-2000
DEFINITION EST382232 MAGE resequences, MAGK Homo sapiens cDNA, mRNA sequence.
ACCESSION AW970151
VERSION AW970151.1 GI:8159996
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 680)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,
I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeaman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 273
Seq primer: Forward
Location/Qualifiers
1. .680
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGK"
/note="Vector: pBluescriptSKm"
BASE COUNT 209 a 162 c 134 g 174 t 1 others
ORIGIN
Query Match 20.5%; Score 585; DB 10; Length 680;
Best Local Similarity 96.9%; Pred. No. 9.9e-97;
Matches 628; Conservative 0; Mismatches 16; Indels 4; Gaps 3;

Qy 2053 CTGAATATGTTTCCATCACACAATTTTGTACTTCACTGAATTTCTTCAAAACCATTTGCA 2112
Db 1 CTGAATATGTTTCCATCACACAATTTTGTACTTCACTGAATTTCTTCAAAACCATTTGCA 60

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JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 457.
FEATURES
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            /db_xref="taxon:9606"
            /clone="IMAGE:2772915"
            /clone_lib="NCI CGAP Kid11"
            /lab_host="DH10B"
            /note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."
BASE COUNT 137 a 85 c 115 g 173 t
ORIGIN
    Query Match 17.4%; Score 497; DB 10; Length 510;
    Best Local Similarity 99.0%; Pred. No. 1.1e-80;
    Matches 500; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2319 CTTTCTCGAGTGATCTAAGAGCCAGATTCTATCTGCACAAATACGTGGTGTCTACTTT 2378
Db 510 CTTTCTCGAGTGATCTAAGAGCCAGATTCTATCTGCACAAATACGTGGTGTCTACTTT 451
Qy 2379 AGAGAGATTGATACAAAGACGATTACATGCTCTCAGTGTCTGCCCAAGTACACATTC 2438
Db 450 AGAGAGATTGATACAAAGACGATTACATGCTCTCAGTGTCTGCCCAAGTACACATTC 391
Qy 2439 ATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCGGTGTCAGCA 2498
Db 390 ATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCGGTGTCAGCA 331
Qy 2499 GGAAAAAGATCAAGCCTGCCACGATGGCTGCTGCTCTTGTAGCCCAACCCATGAGAAG 2558
Db 330 GGAAAAAGATCAAGCCTGCCACGATGGCTGCTGCTCTTGTAGCCCAACCCATGAGAAG 271
Qy 2559 CAAGAGACCTTAAAGCTTCTTATCCCAATATACAGGGAAAAAAGCGTGTGATGATCT 2618
Db 270 CAAGAGACCTTAAAGCTTCTTATCCCAATATACAGGGAAAAAAGCGTGTGATGATCT 211
Qy 2619 GAAGCTTACTATGACGCTTACAAACAGCGCTTAGTAATTAACCAATTTTATACCAATAAA 2678
Db 210 GAAGCTTACTATGACGCTTACAAACAGCGCTTAGTAATTAACCAATTTTATACCAATAAA 151
Qy 2679 TTTTCAAAATATTACTAACTAATGTAGCAATTAACAGATTGGAAACTACATTTTACAAC 2738
Db 150 TTTTCAAAATATTACTAACTAATGTAGCAATTAACAGATTGGAAACTACATTTTACAAC 91
Qy 2739 TCAAGCTGTTTTATACATAGAAATCAATACAGCTTTAATTAAGAAACCTGTAACCATTT 2798
Db 90 TCAAGCTGTTTTATACATAGAAATCAATACAGCTTTAATTAAGAAACCTGTAACCATTT 31
Qy 2799 GATAATGCAACAAATAAGCATCTTC 2823
Db 30 GATAATGCAACAAATAAGCATCTTC 6
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            /tissue_type="carcinoid"
            /lab_host="DH10B"
            /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI_CGAP Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (cloneIDs
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 132 a 84 c 113 g 180 t
ORIGIN
    Query Match 17.3%; Score 493; DB 12; Length 509;
    Best Local Similarity 98.0%; Pred. No. 6.1e-80;
    Matches 499; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 2326 GCAGTGATCTTAAGAGCCAGATTCTATCTGCACAAATACGTGGTGTCTACTTTAGAGAGA 2385
Db 509 GCAGTGATCTTAAGAGCCAGATTCTATCTGCACAAATACGTGGTGTCTACTTTAGAGAGA 450
Qy 2386 TTGTATACAAAAGACGATTACATGCTCTCAGTGTCTGCCCAAGTACCACTTCATGAAGG 2445
Db 449 TTGTATACAAAAGACGATTACATGCTCTCAGTGTCTGCCCAAGTACCACTTCATGAAGG 390
Qy 2446 ATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGACAGGAAAAA 2505
Db 389 ATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGACAGGAAAAA 330
Qy 2506 GATCACAAGCTGCGACGATGGCTGCTCTCTTGTAGCCCAACCCATGAGAAGCAAGAGA 2565
Db 329 GATCACAAGCTGCGACGATGGCTGCTCTCTTGTAGCCCAACCCATGAGAAGCAAGAGA 270
Qy 2566 CCTTAAAGGCTTCTTATCCCAACCAATTACAGGGAAAAAAGCTGTGATGATCCTGAAGCTT 2625
Db 269 CCTTAAAGGCTTCTTATCCCAACCAATTACAGGGAAAAAAGCTGTGATGATCCTGAAGCTT 210
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Qy	2626	ACTATGCAGCCTCAAAACAGCCTTAGTAATTAATAAACATTTTATACCAATAAAATTTTCAA	2685
Db	209	ACTATGCAGCCTCAAAACAGCCTTAGTAATTAATAAACATTTTATACCAATAAAATTTTCAA	150
Qy	2686	ATATTACTTAACCTAATGTAGCAATTAACCTAAGCTTGGAACTACATTTTACAACTTTCAAGC	2745
Db	149	ATATTGCTTAACCTAATGTAGCAATTAACCTAAGCTTGGAACTACATTTTACAACTTTCAAGC	90
Qy	2746	TGTTTTATACATAGAAATCAATTAACGCTTTAAATGGAAACTGTAAACCATTTTGATAATG	2805
Db	89	TGTTTTATACATAGAAATCAATTAACGCTTTAAATGGAAACTGTAAACCATTTTGATAATG	30
Qy	2806	CAACAATAAGCATCTTCCAAAAA 2834	
Db	29	CAACAATAAGCATCTTCCAGCCAAACAAA 1	
RESULT 12			
BE4656508/c			
LOCUS	BE4656508	502 bp	mRNA
DEFINITION	hx93h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3195409 3', mRNA sequence.		
ACCESSION	BE4656508		
VERSION	BE4656508.1		
KEYWORDS	GI:9512206		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 502)		
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: qgabs-t@mail.nih.gov		
	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.		
	cDNA Library Preparation: M. Bento Soares, Ph.D.		
	cDNA Library Arrayed by: Greg Lennon, Ph.D.		
	DNA Sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: infoimage.llnl.gov		
FEATURES	Seq primer: -40UP from Gibco		
source	High quality sequence stop: 466.		
	Location/Qualifiers		
	1. 502		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:3195409"		
	/clone_lib="NCI_CGAP_Kid11"		
	/lab_host="DH10B"		
	/note="Organ: kidney; Vector: pTV73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	130 a	87 c	114 g 171 t
ORIGIN			
Query Match	16.7%; Score 477.4; DB 10; Length 502;		
Best Local Similarity	97.8%; Pred No. 4.3e-77;		
Matches 484; Conservative	0; Mismatches 11; Indels 0; Gaps 0;		
Qy	2327	CAGTGATCTTAAGAGCCAGATTCATCTGCACAAATACGTGCTGCTACTTTAGAGAGAT	2386

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 151 a 136 c 166 g 162 t

ORIGIN

Query Match 16.7%; Score 476.8; DB 10; Length 615;
Best Local Similarity 84.8%; Pred. No. 5.1e-77;
Matches 599; Conservative 0; Mismatches 12; Indels 95; Gaps 2;

QY 1491 TGTACCTGTGTAGATGACCTAGCCCTTTAGGTAAGCGAACTGTATGTAGTAACCT 1550
Db 1 TCTACCTGTGTAGATGACCTAGCCCTTTAGGTAAGCGAACTGTATGTAGTAACCT 60
QY 1551 GTACAAAGTTTAGGTTACAGACCCCGGAGTCTTGGGCATGTGGTCTCGGTCACCTGGTT 1610
Db 61 GTACAAAGTTTAGGTTACAGACCCCGGAGTCTTGGGCATGTGGTCTCGGTCACCTGGTT 120
QY 1611 TTGACTTTAGGGCTTTGTTACAGATGTGTGACCAAGGGAATAATGTCATGACAACTA 1670
Db 121 TTGACTTTAGGGCTTTGTTACAGATGTGTGACCAAGGGAATAATGTCATGACAACTA 180
QY 1671 GAGGTAGGGCGGAAGCCAGAAAGGAAGTTTGGCTGAAGTAGGAGTCTTGGTGAGA 1730
Db 181 GAGGTAGGGCGGAAGCCAGAAAGGAAGTTTGGCTGAAGTAGGAGTCTTGGTGAGA 233
QY 1731 TTTTGTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1790
Db 234 ----- 233
QY 1791 TATTTTCTTACTTTGGGAGCGACTGCATCCGACATPAAAGGAACAGTTGTGTCTGCCCCA 1850
Db 234 -----GCGACTGCATCCGACATPAAAGGAACAGTTGTGTCTGCCCCA 274
QY 1851 CAAAGGCGTCCCTTCCCTCTGGATACAAACAAAGCAAGCCGGAGGCTGGTGGCT 1910
Db 275 CAAAGGCGTCCCTTCCCTCTGGATACAAACAAAGCAAGCCGGAGGCTGGTGGCT 334
QY 1911 CTCCTCTCTGTCTGTCTGTGTGGCCACATGGTGTCTGGTGGAGGATCTATCTAATG 1970
Db 335 CTCCTCTCTGTCTGTCTGTGTGGCCACATGGTGTCTGGTGGAGGATCTATCTAATG 394
QY 1971 TGGAGGACGAAAGGATCAAGAAAGCTTCTTTTTCACCAACACACTACTGCCCCCAAT 2030
Db 395 TGGAGGACGAAAGGATCAAGAAAGCTTCTTTTTCACCAACACACTACTGCCCCCAAT 454
QY 2031 AAGGTTCTGT 2090
Db 455 AAGGTTCTGT 514
QY 2091 GAATTTCTTCAAAACCATTTGCAGAGTGAAGTCACTCTTGAAGAGTGGCAGAAAAAGAAA 2150
Db 515 GAATTTCTTCAAAACCATTTGCAGAGTGAAGTCACTCTTGAAGAGTGGCAGAAAAAGAAA 565
QY 2151 ATAGCAGAGTGGTCCAGTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2196
Db 566 GTAGCAGAGTGGTCCAGTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 611

RESULT 14
BF064177/c
LOCUS 7h95b11.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:3323709 3',
DEFINITION mRNA sequence.
ACCESSION BF064177
VERSION BF064177.1 GI:10823087
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 484)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ilian Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 400.
Location/Qualifiers
1..484
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/clone="IMAGE:3323709"
/clone_lib="NCI_CGAP Col6"
/tissue_type="Colon Tumor, RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP Col6 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 121 a 95 c 120 g 148 t
ORIGIN

Query Match 16.6%; Score 475.2; DB 12; Length 484;
Best Local Similarity 99.4%; Pred. No. 1.1e-76;
Matches 477; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2220 CTTTCCATGACGTCAACAGTGTGCGATGTGACCTGTGCGAAGAGGAGGAGTCC 2279
Db 484 CTTTCCATGACGTCAACAGTGTGCGATGTGACCTGTGCGAAGAGGAGGAGTCC 425
QY 2280 AGTGAGAACTCTCAAGACCTCTTCCCTTTCACCTTTTTCAGTGATCTAAGA 2339
Db 424 AGTGAGAACTCTCAAGACCTCTTCCCTTTCACCTTTTTCAGTGATCTAAGA 365
QY 2340 AGCCAGATTCTGTGCAAAATAGTGTGTCTTCTTAGAGAGATTGATACAAAGAC 2399
Db 364 AGCCAGATTCTGTGCAAAATAGTGTGTGTCTTCTTAGAGAGATTGATACAAAGAC 305
QY 2400 GATTACATGCTCTCAGTGTCTGCCCAAGTACCACCTTCATGAAGGATGCCACTTTC 2459
Db 304 GATTACATGCTCTCAGTGTCTGCCCAAGTACCACCTTCATGAAGGATGCCACTTTC 245
QY 2460 TGTGAGAACTTCTCCATGTCAAGCAGCAGGTGTGTCAGGAGGAGGAGGAGGAGGAGGAG 2519
Db 244 TGTGAGAACTTCTCCATGTCAAGTACAGGTGTGTCAGGAGGAGGAGGAGGAGGAGGAG 185
QY 2520 CACATGGCTGCTGCTCTTGTAGCCACCCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 2579
Db 184 CACATGGCTGCTGCTCTTGTAGCCACCCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 125
QY 2580 TATCCCACTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2639
Db 124 TATCCCACTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 65
QY 2640 AAACAGCCTTAGTAATTAACATTTTATACCAATAAAATTTTCAAAATATTACTAACTAA 2699
Db 64 AAACAGCCTTAGTAATTAACATTTTATACCAATAAAATTTTCAAAATATTACTAACTAA 5

RESULT 15
AAS14396/c

LOCUS AA514396 488 bp mRNA. linear EST 18-AUG-1997
DEFINITION nf57c01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:924000 3',
mRNA sequence.
ACCESSION AA514396
VERSION AA514396.1 GI:2253996
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 488)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 873 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 475.
FEATURES
Location/Qualifiers
1..488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:924000"
/clone.lib="NCI_CGAP_Co3"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library went through one round of
normalization."
BASE COUNT 130 a 81 c 109 g 168 t
ORIGIN
Query Match 16.6%; Score 475; DB 9; Length 488;
Best Local Similarity 99.0%; Pred. No. 1.2e-76;
Matches 478; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2341 GCAGATTCATCGACAATACGGTGGTCTTACTTTAGAGAGATTGATACAAAGACG 2400
DB 488 GCAGATTCATCGACAATACGGTGGTCTTACTTTAGAGAGATTGATACAAAGACG 429
QY 2401 ATTACAATGCTCTCAGTGTCTGCCCAAGTACCACCTTCATGAAGGATGCCACTGTTTCT 2460
DB 428 ATTACAATGCTCTCAGTGTCTGCCCAAGTACCACCTTCATGAAGGATGCCACTGTTTCT 369
QY 2461 GTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGACAGAGAAAAGATCACAAGCCTGCC 2520
DB 368 GTGCAGAACTTCTCCATGTCAAGTACAGGTGTGACAGAGAAAAGATCACAAGCCTGCC 309
QY 2521 ACGATGGCTGCTGCTCTTGTAGCCACCATGAGAGAACAGACCTTTAAAGGCTTCT 2580
DB 308 ACGATGGCTGCTGCTCTTGTAGCCACCATGAGAGAACAGACCTTTAAAGGCTTCT 249
QY 2581 ATCCCAACCAATTACAGGGGAAAAAAGCTGTGATGATCCTCTCAAGCTTACTATGAGCCTACA 2640
DB 248 ATCCCAACCAATTACAGGGGAAAAAAGCTGTGATGATCCTCTCAAGCTTACTATGAGCCTACA 189
QY 2641 AACAGCCTTAGTAATTAATAAACAATTTTATACCAATAAATTTTCAAAATATTACTACTAAT 2700

DB 188 AACAGCCTTAGTAATTAATAAACAATTTTATACCAATAAATTTTCAAAATATTGCTAACTAAT 129
QY 2701 GTAGCATTAACTAACGATTGGAAACTTACATTTTCAAACTTCAAAAGCTGTTTATACATAGA 2760
DB 128 GTAGCATTAACTAACGATTGGAAACTTACATTTTCAAACTTCAAAAGCTGTTTATACATAGA 69
QY 2761 AATCAATTACAGCTTTAATTGAAAACTGTAAACATTTTGTATTAATGCAACAATAAAGCATC 2820
DB 68 AATCAATTACAGCTTTAATTGAAAACTGTAAACATTTTGTATTAATGCAACAATAAAGCATC 9
QY 2821 TTC 2823
DB 8 TTC 6

Search completed: May 28, 2003, 10:13:11
Job time : 3998.87 secs

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Result No.	Query	Score	Query			Description	
			Match	Length	ID		
C	1	2855	100.0	2856	10	US-09-778-871-2	Sequence 2, Appli
	2	1178.8	41.3	32177	9	US-09-764-891-8062	Sequence 8062, Ap
	3	1078	37.7	1827	10	US-09-778-371-1	Sequence 1, Appli
	4	1041.8	36.5	1796	9	US-09-863-818A-1	Sequence 1, Appli
	5	1040.2	36.4	1841	10	US-09-886-404-17	Sequence 17, Appl
	6	1040.2	36.4	2015	10	US-09-886-404-19	Sequence 19, Appl
	7	763.4	26.7	1515	9	US-09-874-503-11	Sequence 11, Appl
	8	763.4	26.7	1515	9	US-10-000-157-11	Sequence 11, Appl
	9	763.4	26.7	1515	9	US-10-063-547-157	Sequence 157, App
	10	763.4	26.7	1515	9	US-09-747-259-11	Sequence 11, Appl
11	763.4	26.7	1515	9	US-10-174-590-399	Sequence 399, App	
12	763.4	26.7	1515	9	US-10-176-758-399	Sequence 399, App	
13	763.4	26.7	1515	9	US-10-063-616-157	Sequence 157, App	
14	763.4	26.7	1515	9	US-10-175-737-399	Sequence 399, App	
15	763.4	26.7	1515	9	US-10-063-502-157	Sequence 157, App	
16	763.4	26.7	1515	9	US-10-173-766-399	Sequence 399, App	
17	763.4	26.7	1515	9	US-10-175-738-399	Sequence 399, App	
18	763.4	26.7	1515	9	US-10-175-752-399	Sequence 399, App	
19	763.4	26.7	1515	9	US-10-176-482-399	Sequence 399, App	

Qy 181 CAGGGACTATTCAATTTTGATGAATGTAAGCTGGTACTCCGGGCAGATGCCAGCATCC 240

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

QY 241 GCTTGTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTCTACAGCT 300
DB 241 GCTTGTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTCTACAGCT 300
QY 301 GTGTGAGGTGCAATTACACAGAGCCCTTCAGACTCAGACAGACCCCTCTGGTGGTAAT 360
DB 301 GTGTGAGGTGCAATTACACAGAGCCCTTCAGACTCAGACAGACCCCTCTGGTGGTAAT 360
QY 361 GGACATTTTCTATATATCGGCTTCCCTGTAGAGCTGACACAGACTATTTTCAATTTGGGGCCC 420
DB 361 GGACATTTTCTATATCGGCTTCCCTGTAGAGCTGACACAGACTATTTTCAATTTGGGGCCC 420
QY 421 ATAATATTCCTAAATGCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAAATTCACCT 480
DB 421 ATAATATTCCTAAATGCAAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAAATTCACCT 480
QY 481 CACGAGCTGCTAGACCAATATGAATATATAAAAAAGTGTGTCAAGGCCGGAAGCC 540
DB 481 CACGAGCTGCTAGACCAATATGAATATATAAAAAAGTGTGTCAAGGCCGGAAGCC 540
QY 541 TGTGGGATCCGAACATCACTGCTTGTGAAGAAATAGAGGAGACAGTAGAAGTGAATTTCA 600
DB 541 TGTGGGATCCGAACATCACTGCTTGTGAAGAAATAGAGGAGACAGTAGAAGTGAATTTCA 600
QY 601 CAACCACTCCCTGGGAAACAGATACATGCTCTTATCCAAACAGCACTATCATCGGCT 660
DB 601 CAACCACTCCCTGGGAAACAGATACATGCTCTTATCCAAACAGCACTATCATCGGCT 660
QY 661 TTTCTCAGGTGTTGAGCCACACAGAAACAAACGCGAGCTTCAGTGGTGAATCCAG 720
DB 661 TTTCTCAGGTGTTGAGCCACACAGAAACAAACGCGAGCTTCAGTGGTGAATCCAG 720
QY 721 TGACTGGGATAGTGAAGGTGCTACGCTGCGAGGTAAAGTTCACTGAGCTGCTCTGGGGAG 780
DB 721 TGACTGGGATAGTGAAGGTGCTACGCTGCGAGGTAAAGTTCACTGAGCTGCTCTGGGGAG 780
QY 781 GGAAGGACATAGAAGACTGTTCATCATTTTAAAGGATGAGTTCTCTCTGT 840
DB 781 GGAAGGACATAGAAGACTGTTCATCATTTTAAAGGATGAGTTCTCTCTGT 840
QY 841 CAAATGCACTTCTGCCAGCAGACACAGATTAAAGTGGGTTTCAAGGGGTTCTTTCGCTGC 900
DB 841 CAAATGCACTTCTGCCAGCAGACACAGATTAAAGTGGGTTTCAAGGGGTTCTTTCGCTGC 900
QY 901 AGCCTCCACCGTCTGAGGTGACGAGCCGACGCTGCGAGTTGCTGCTTGTGCTTGTGA 960
DB 901 AGCCTCCACCGTCTGAGGTGACGAGCCGACGCTGCGAGTTGCTGCTTGTGCTTGTGA 960
QY 961 TTAATGGCTGCTGACCTTCCAAAGCACTTTTATTTTCACTTCTGTCAACACTCAG 1020
DB 961 TTAATGGCTGCTGACCTTCCAAAGCACTTTTATTTTCACTTCTGTCAACACTCAG 1020
QY 1021 GGATAGCAGTACATTTTACTTCCGAAGCTTTTAACTGCAAGATGAAGTGCAGAGGTT 1080
DB 1021 GGATAGCAGTACATTTTACTTCCGAAGCTTTTAACTGCAAGATGAAGTGCAGAGGTT 1080
QY 1081 TTAATGGGAGGTTTGAAGTCCAGCAGCGTATGAACTCTGAGAGGGGCTGCCAGTC 1140
DB 1081 TTAATGGGAGGTTTGAAGTCCAGCAGCGTATGAACTCTGAGAGGGGCTGCCAGTC 1140
QY 1141 CTCTCGGGCCGAGCGGACCCAGCTGGAACACAGGAAGTTGGAGCAGTAGTGTCTCTT 1200
DB 1141 CTCTCGGGCCGAGCGGACCCAGCTGGAACACAGGAAGTTGGAGCAGTAGTGTCTCTT 1200
QY 1201 CACCTCTCAGTATGCTCTTTTAACTCTAGTTTGAAGTGGGACACAGGAAGTCCAGT 1260
DB 1201 CACCTCTCAGTATGCTCTTTTAACTCTAGTTTGAAGTGGGACACAGGAAGTCCAGT 1260
QY 1261 GGGGACACAGCCACTCCCAAGAAATAGCAACTTCCATGCTTCACTCCCTGCGATAAA 1320
DB 1261 GGGGACACAGCCACTCCCAAGAAATAGCAACTTCCATGCTTCACTCCCTGCGATAAA 1320
QY 1321 AGTGNTCAAACACACAGAGGGGGCAGGCCACCGAGGGTATGATGGGTACTACCTTTT 1380

DB 1321 AGTGNTCAAACACACAGAGGGGGCAGGCCACCGAGGGTATGATGGGTACTACCTTT 1380
QY 1381 TCTGGAGAACCATAGACTTCCCTTACTACAGGACTTGCATGCTCCTAAAGCACTGGCTGA 1440
DB 1381 TCTGGAGAACCATAGACTTCCCTTACTACAGGACTTGCATGCTCCTAAAGCACTGGCTGA 1440
QY 1441 AGGAAGCCAGAGGATCACTGCTGCTCCTTTTGTAGAGGAAATGTTTGTGACCTGGT 1500
DB 1441 AGGAAGCCAGAGGATCACTGCTGCTCCTTTTGTAGAGGAAATGTTTGTGACCTGGT 1500
QY 1501 AAGATATGACCTAGCCCTTTTAGGTAAAGGAACTGCTATGTTAGTAACCTGTACAAAGTT 1560
DB 1501 AAGATATGACCTAGCCCTTTTAGGTAAAGGAACTGCTATGTTAGTAACCTGTACAAAGTT 1560
QY 1561 TAGGTTACAGACCCCGGAGCTTTGGGCACTGTGGGTCTCCGGTCACTGTTTTCACCTTAG 1620
DB 1561 TAGGTTACAGACCCCGGAGCTTTGGGCACTGTGGGTCTCCGGTCACTGTTTTCACCTTAG 1620
QY 1621 GGCTTTGTACAGATGCTGACCAAGGGGAAATGTGATGACAACTAGAGGTAGGGG 1680
DB 1621 GGCTTTGTACAGATGCTGACCAAGGGGAAATGTGATGACAACTAGAGGTAGGGG 1680
QY 1681 CGAAGCCAGAAAGAGGAAAGTTTGGCTGAAAGTAGGAGTCTTGGTGAATTTTGTCTGTG 1740
DB 1681 CGAAGCCAGAAAGAGGAAAGTTTGGCTGAAAGTAGGAGTCTTGGTGAATTTTGTCTGTG 1740
QY 1741 ATGCATGTTGTAACCTTCTGAGCCCTTGTGTTTCTCAGCTGACTCATATTTTCTTA 1800
DB 1741 ATGCATGTTGTAACCTTCTGAGCCCTTGTGTTTCTCAGCTGACTCATATTTTCTTA 1800
QY 1801 CTTTGGGAGCAGCTGACATCCGACATAAAGGAACTGCTGCTCTGCCACAAACAGGGG 1860
DB 1801 CTTTGGGAGCAGCTGACATCCGACATAAAGGAACTGCTGCTCTGCCACAAACAGGGG 1860
QY 1861 TCCCTTTCTCTGGATAACAAACAAAGCAAGCCGGGAGGCTGGCTGCTCTCTCTGC 1920
DB 1861 TCCCTTTCTCTGGATAACAAACAAAGCAAGCCGGGAGGCTGGCTGCTCTCTCTGC 1920
QY 1921 TGTCTCTGCTGGTGGCCACATGGGTGCTGGTGGAGGATCTATCTAATGTGGAGGACG 1980
DB 1921 TGTCTCTGCTGGTGGCCACATGGGTGCTGGTGGAGGATCTATCTAATGTGGAGGACG 1980
QY 1981 AAAGATCAAGAGACTTCTCTTTTACCACTACTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
DB 1981 AAAGATCAAGAGACTTCTCTTTTACCACTACTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
QY 2041 TGGTTTACCCATCTGAAATATGTTTCTCATCACAATTTGTTTACTTCACTGAATTTCTTC 2100
DB 2041 TGGTTTACCCATCTGAAATATGTTTCTCATCACAATTTGTTTACTTCACTGAATTTCTTC 2100
QY 2101 AAAACCATTCAGAGTGAAGTCACTCTTGAAGTGGCAGAAAAGAAAATAGCAGAGA 2160
DB 2101 AAAACCATTCAGAGTGAAGTCACTCTTGAAGTGGCAGAAAAGAAAATAGCAGAGA 2160
QY 2161 TGGGTCAGTGCAGTGGCTTGCCTCAAAAGAGGAGCAGACAAAGTCTCTCTCTTC 2220
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QY 2221 TTTTCAATGACGTCACAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
DB 2221 TTTTCAATGACGTCACAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
QY 2281 GTGAGAACTCTCAAGACCTCTTCCCTTGTCTTAACTTTTCTGCTGCTGCTGCTGCTGCTG 2340
DB 2281 GTGAGAACTCTCAAGACCTCTTCCCTTGTCTTAACTTTTCTGCTGCTGCTGCTGCTGCTG 2340
QY 2341 GCGAATTCATCTGACAAATACGTTGGTGTCTACTTCTAGAGAGATTCATACAAAGAGC 2400
DB 2341 GCGAATTCATCTGACAAATACGTTGGTGTCTACTTCTAGAGAGATTCATACAAAGAGC 2400
QY 2401 ATTACAATGCTCTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 2460

Db	2401	ATTACAATGCTCTCAGTGTCTGCCCAAGTACCACCTTCATGAAGATGCCACTGCTTTCT	2460
Qy	2461	GTGCAGAACTTCTCCATGTCGAAGCAGCAGGTGTGACGAGGAAAAAGATCACAAGCTGC	2520
Db	2461	GTGCAGAACTTCTCCATGTCGAAGCAGCAGGTGTGACGAGGAAAAAGATCACAAGCTGC	2520
Qy	2521	ACGATGGCTGTCTCCCTGTGTAGCCACCCATGAGAGCGAGAGACCTTAAAGGCTTCT	2580
Db	2521	ACGATGGCTGTCTCCCTGTGTAGCCACCCATGAGAGCGAGAGACCTTAAAGGCTTCT	2580
Qy	2581	ATCCACCAATTACAGGGAAAAAAGCTGTGATGATCTCTGAAGCTTACTATGCAGCCTACA	2640
Db	2581	ATCCACCAATTACAGGGAAAAAAGCTGTGATGATCTCTGAAGCTTACTATGCAGCCTACA	2640
Qy	2641	AACGCTTTAGTAATTAATAACAATTATTAACCAATAAAATTTTCAAATATTTACTAACTAAT	2700
Db	2641	AACGCTTTAGTAATTAATAACAATTATTAACCAATAAAATTTTCAAATATTTACTAACTAAT	2700
Qy	2701	GTAGCATTAACCTAACGATTGGAACTACATTTACAACTTCAAGCTGTTTATATACATAGA	2760
Db	2701	GTAGCATTAACCTAACGATTGGAACTACATTTACAACTTCAAGCTGTTTATATACATAGA	2760
Qy	2761	AATCAATTTACAGCTTTAATTGAAAACCTGTAACTTTTGATTAATGCAACAATAAAGCATC	2820
Db	2761	AATCAATTTACAGCTTTAATTGAAAACCTGTAACTTTTGATTAATGCAACAATAAAGCATC	2820
Qy	2821	TTCCAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2856
Db	2821	TTCCAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2856

RESULT 2

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US-09-764-891-8062/c
; Sequence 8062, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8062
; LENGTH: 32177
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8062

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Query Match      41.3%; Score 1178.8; DB 9; Length 32177;
Best Local Similarity 98.0%; Pred. No. 8.4e-305;
Matches 1203; Conservative 0; Mismatches 23; Indels 1; Gaps 1;
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Qy	663	TCTCAGTGTTTGAGCCACACAGAAACAAACGGAGCTTCAGTGGTGATTCCAGTG	722
Db	24552	TCTCTCTCTTAAAGCCACACAGAAACAAACGGAGCTTCAGTGGTGATTCCAGTG	24493
Qy	723	ACTGGGGATAGTGAAGTGCTACGGTCAGGTAAGTTCACTGAGCTGCTCTGGGGAGGG	782
Db	24492	ACTGGGGATAGTGAAGTGCTACGGTCAGGTAAGTTCACTGAGCTGCTCTGGGGAGGG	24433
Qy	783	AAGGGACATAGAAGACTGTTTCCATCTCATTTGCTTTAAGGATGAGTTCTCTTGTCA	842
Db	24432	AAGGGACATAGAAGACTGTTTCCATCTCATTTGCTTTAAGGATGAGTTCTCTTGTCA	24373
Qy	843	AATSCACTTCTGCCAGCAGACACACAGTTAAGTGGCGTTCACTGGGGTCTTTCCCTCGAG	902
Db	24372	AATGCATCTTCGCCAGCAGACACACAGTTAAGTGGCGTTCACTGGGGTCTTTCCCTCGAG	24313
Qy	903	CCTCCACCGTCTCAGGTCAGGAGCCGACGTGGCAGTTGTGGTCCCTTTTGGCTTGATT	962
Db	24312	CCTCCACCGTCTCAGGTCAGGAGCCGACGTGGCAGTTGTGGTCCCTTTTGGCTTGATT	24253

Db	1530	CAAGAGACCTTAAAGGCTTCCTATCCACCATTACAGGGAACGCTGTGATGTCCT	1589
Qy	2619	GAAGCTTACTATCAGCGCTACAACAGCGCTTAGTAATTAAAACATTTTATACCAATAAAA	2678
Db	1590	GAAGCTTACTATCAGCGCTACAACAGCGCTTAGTAATTAAAACATTTTATACCAATAAAA	1649
Qy	2679	TTTTCAAAATATTACTAACTAATGTAGCATTTACTAACGATTCGGAACCTACATTTACAACCT	2738
Db	1650	TTTTCAAAATATTACTAATGTAGCATTTACTAACGATTCGGAACCTACATTTACAACCT	1709
Qy	2739	TCAAAGCTGTTTTATACATAGAAATCAATTTACAGCTTTTAATTTGAAACCTGTAAACCATTTT	2798
Db	1710	TCAAAGCTGTTTTATACATAGAAATCAATTTACAGCTTTTAATTTGAAACCTGTAAACCATTTT	1769
Qy	2799	GATAATGCACAATAAAGCATCTTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	2856
Db	1770	GATAATGCACAATAAAGCATCTTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	1827

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RESULT 4
US-09-863-818A-1
; Sequence 1, Application US/09863818A
; Publication No. US20030092881A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K
; CURRENT APPLICATION NUMBER: US/09/863,818A
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(1509)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (46)..()
; OTHER INFORMATION:
US-09-863-818A-1

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Db	748	CAGCTGACCTCCATATTTTCTACTGTGGCAGCGACTGCATCCGACATATAAGGACAGTT	807		
Qy	1839	GTGCTCTGCCCCAACAAACAGCGCTCCCTTTCCTCTGGATAACAAACAAAGCAGCGCGGA	1898		
Db					
Db	808	GTGCTCTGCCCCAACAAACAGCGCTCCCTTTCCTCTGGATAACAAACAAAGCAGCGCGGA	867		
Qy	1899	GGCTGGCTGCCTCTCCTCTGCTGTCCTGTGCTGGTGCCACATGGGTGTGTGTGGCAGGG	1958		
Db					
Db	868	GGCTGGCTGCCTCTCCTCTGCTGTCCTGTGCTGGTGCCACATGGGTGTGTGTGGCAGGG	927		
Qy	1959	ATCTATCTAATGTGGAGGACGAAAGGATCAAGAGACTTCCTTTTCTACACACACACTA	2018		
Db					
Db	928	ATCTATCTAATGTGGAGGACGAAAGGATCAAGAGACTTCCTTTTCTACACACACACTA	987		
Qy	2019	CTGCCCCCACTTAAGGTTCCTGTGGTFTTACCACATCTGAAATATGTTTCCATCACACAAT	2078		
Db					
Db	988	CTGCCCCCACTTAAGGTTCCTGTGGTFTTACCACATCTGAAATATGTTTCCATCACACAAT	1047		
Qy	2079	TGTTACTTCACTGAATTTCTTCAAAACCAATTCGACAGTGTAGGTGATCTTGAAAGTGG	2138		
Db					
Db	1048	TGTTACTTCACTGAATTTCTTCAAAACCAATTCGACAGTGTAGGTGATCTTGAAAGTGG	1107		


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; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovaanik, Melissa.
; APPLICANT: Vanlookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P.Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381C1P4 (US)
; CURRENT APPLICATION NUMBER: US/10/000,157
; CURRENT FILING DATE: 2001-10-30
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/172096
; PRIOR FILING DATE: 1999-12-23
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; PRIOR APPLICATION NUMBER: 60/191007
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; PRIOR FILING DATE: 2001-03-22
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; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/908827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/931836
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/31274

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; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15364
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 11
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-000-157-11

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Query Match      26.7%; Score 763.4; DB 9; Length 1515;
Best Local Similarity 99.9%; Pred. No. 3.3e-194;
Matches 764; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1779 CAGCTGACTCCATATTTTCTTACTTGTGCGAGCGACTGCATCCGACATAAAGGAACAGTT 1838
Db 751 CAGCTGACTCCATATTTTCTTACTTGTGCGAGCGACTGCATCCGACATAAAGGAACAGTT 810

Qy 1839 GTGCTCTGCCCCAACAAAGGGGTCCTTTCCCTCTGGATAACAAACAAAGCAAGCGGGA 1898
Db 811 GTGCTCTGCCCCAACAAAGGGGTCCTTTCCCTCTGGATAACAAACAAAGCAAGCGGGA 870

Qy 1899 GGCTGGCTGCCTCTCTCCTCTGCTGTCTCTGCTGGGCCACATGGGTGCTGGTGCAGGG 1958
Db 871 GGCTGGCTGCCTCTCTCCTCTGCTGTCTCTGCTGGGCCACATGGGTGCTGGTGCAGGG 930

Qy 1959 ATCTATCTAATGTGAGGCACGAAAGGATCAAGAGACTTCCTTTTCTACCAACACACTA 2018
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Qy 2019 CTGCCCCCCCATTAAAGTTCTTTGTGGTTTACCCATCTGAAATATGTTTCCATCACA 2078
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Qy 2079 TGTACTTCACTGAATTTCTTCAAAACCATTGCGAGAAGTGAGGTCACTCTTGAAGTGG 2138
Db 1051 TGTACTTCACTGAATTTCTTCAAAACCATTGCGAGAAGTGAGGTCACTCTTGAAGTGG 1110

Qy 2139 CAGAAAAAGAAAATAGCAGAGATGGTCCAGTGCAGTGGCTTGCCACTCAAAAGAGCA 2198
Db 1111 CAGAAAAAGAAAATAGCAGAGATGGTCCAGTGCAGTGGCTTGCCACTCAAAAGAGCA 1170

Qy 2199 GCAGACAAAGTCGTCTTCTTCTTCCAAATGACGTCACACAGTGTGCGATGGTACCTGT 2258
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Qy 2259 GCGAAGACGAGGGCAGTCCCGACGAGAACTCTCAAGACCTCTTCCCTCCCTTTTAAAC 2318

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Query Match	26.7%	Score 763.4	DB 9	Length 1515
Best Local Similarity	99.9%	Pred. No. 3.3e-194		
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DB 751	CAGCTGACTCCATATTTTCCTACTGTGTGGCAGCGACTGCATCCGACATAAAGCAACAGTT	810		
QY 1839	GTGCTCTGCCCAAAAACAGGCGTCCCTTTCCTCTGGATAACAAACAAAGCAAGCGGGA	1898		
DB 811	GTGCTCTGCCCAAAAACAGGCGTCCCTTTCCTCTGGATAACAAACAAAGCAAGCGGGA	870		
QY 1899	GGCTGGCTGCCTCTCCCTCCTGCTGTCTGTGTGGCCACATGGGTGCTGTGGCAGGG	1958		
DB 871	GGCTGGCTGCCTCTCCCTCCTGCTGTCTGTGTGGCCACATGGGTGCTGTGGCAGGG	930		
QY 1959	ATCTATCTAATGTGGAGGCACAAAGGATCAAGAAGACTTCCTTTTACACACACACTA	2018		
DB 931	ATCTATCTAATGTGGAGGCACAAAGGATCAAGAAGACTTCCTTTTACACACACACTA	990		
QY 2019	CTGCCCCCATTAAGGTTCTTGTGGTTTACCACATCTGAATAATGTTTCCATCACACAAT	2078		
DB 991	CTGCCCCCATTAAGGTTCTTGTGGTTTACCACATCTGAANAATGTTTCCATCACACAAT	1050		
QY 2079	TGTTTACTTCACTGAATTTCTTCAAAACCAATTCGAGAAGTGAGGTCATCCTTGAAGAATGG	2138		
DB 1051	TGTTTACTTCACTGAATTTCTTCAAAACCAATTCGAGAAGTGAGGTCATCCTTGAAGAATGG	1110		
QY 2139	CAGAAAAGAAAATAGCAGAGATGGTCCAGTGCAGTGGCTTGCACACTCAAAAAGAGGCA	2198		
DB 1111	CAGAAAAGAAAATAGCAGAGATGGTCCAGTGCAGTGGCTTGCACACTCAAAAAGAGGCA	1170		
QY 2199	GCAGACAAGTCGCTTCCCTTTCCTTCCAAACGACGTCAACAGTGTGTGGATGGTACCTGT	2258		
DB 1171	GCAGACAAGTCGCTTCCCTTTCCTTTCCTTCCAAATGACGTCAACAGTGTGTGGATGGTACCTGT	1230		
QY 2259	GGCAAGCAGGAGGCGAGTCCCGAGTGAGAACTCTCAAGACCTCTTCCCTCTGCCCTTTAAC	2318		

Query Match	26.7%	Score 763.4	DB 9	Length 1515
Best Local Similarity	99.9%	Pred. No. 3.3e-194		
Matches 764	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy 1779	CAGCTGACTCCATATTTTCCTACTGTGTGGCAGCAGCTGCATCCGACATAAAGGAACAGTT	1838		
Db 751	CAGCTGACTCCATATTTTCCTACTGTGTGGCAGCAGCTGCATCCGACATAAAGGAACAGTT	810		
Qy 1839	GTGCTCTGCCACAAAACAGGGCGTCCCTTTCCCTCTGGATAACAACAAAGCAAGCCGGGA	1898		
Db 811	GTGCTCTGCCACAAAACAGGGCGTCCCTTTCCCTCTGGATAACAACAAAGCAAGCCGGGA	870		
Qy 1899	GGCTGGGTGCCTCTCCTCCTGCTCTCTGCTGGTGGCCACATGGTGCTCGTGGCAGGG	1958		
Db 871	GGCTGGGTGCCTCTCCTCCTGCTCTCTGCTGGTGGCCACATGGTGCTCGTGGCAGGG	930		
Qy 1959	ATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCCTTTCTACCAACACACTA	2018		
Db 931	ATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCCTTTCTACCAACACACTA	990		
Qy 2019	CTGCCCCCAATTAAGTTCTTGTGGTTTACCATCTGAAATATGTTTCCATCAACAATT	2078		
Db 991	CTGCCCCCAATTAAGTTCTTGTGGTTTACCATCTGAAATATGTTTCCATCAACAATT	1050		

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RESULT 13
US-10-063-616-157
; Sequence 157, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 157
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-157

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	Query Match	26.7%	Score 763.4	DB 9	Length 1515	
	Best Local Similarity	99.9%	Pred. No. 3.3e-194			
	Matches 764	Conservative 0	Mismatches 1	Indels 0	Gaps 0	
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Db	751	CAGCTGACTCGATATTTTCTACTTTGGCAGCGACTGCATCCGACATAAAGGAACAGTT	810			
Qy	1839	GTGCTCTGCCACAAAACAGGGCGTCCCTTCCTCTGGATACACAAAAGCAACGCCGGA	1898			
Db	811	GTGCTCTGCCACAAAACAGGGCGTCCCTTCCTCTGGATACACAAAAGCAACGCCGGA	870			
Qy	1899	GGCTGGGTGCCTCTCCCTGCTGCTGTGGTGGCACATGGGTGCTGGTGGCAGGG	1958			

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Job time : 422.392 secs

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GenCore version 5.1.4 p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 23:31:59 ; Search time 94.9423 Seconds
(without alignments)
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Perfect score: 2856
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	1.9	6243	2	US-09-056-075-1
2	50	1.8	19124	2	US-08-487-828B-13
3	49.8	1.7	1776	3	US-08-655-352-10
4	49.8	1.7	1776	4	US-09-258-016-10
5	49.8	1.7	1776	4	US-09-257-825B-10
6	49.4	1.7	240	1	US-08-628-417-6
7	49.2	1.7	1100	4	US-07-861-458C-4
8	49	1.7	2836	3	US-08-747-221B-24
9	49	1.7	2836	3	US-08-747-221B-26
10	49	1.7	2836	4	US-09-005-051-24
11	49	1.7	2836	4	US-09-005-051-26
12	49	1.7	5173	1	US-08-242-677-1
13	48.4	1.7	2447	2	US-09-014-969-14
14	48.2	1.7	991	3	US-08-924-747-25
15	48.2	1.7	991	4	US-09-247-373B-25
16	48.2	1.7	991	4	US-09-296-715-25
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18	47.4	1.7	974	2	US-08-504-459-13
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20	47.4	1.7	1578	4	US-09-664-800-1
21	47.4	1.7	1578	4	US-09-665-309-1
22	47.4	1.7	1578	4	US-09-661-569-1
23	47.4	1.7	1720	4	US-09-227-357-139
24	47.4	1.7	1957	5	PT-US92-06300-1
25	47.2	1.7	593	4	US-09-385-982-262
26	47.2	1.7	658	4	US-08-998-416-595
27	47	1.6	1582	3	US-08-545-196B-10

28	47	1.6	1582	3	US-08-545-196B-12	Sequence 12, Appl
29	47	1.6	2095	4	US-09-227-357-31	Sequence 31, Appl
30	47	1.6	2202	4	US-09-465-558-59	Sequence 59, Appl
c 31	46.4	1.6	602	1	US-08-764-100-8	Sequence 8, Appl
c 32	46.4	1.6	642	1	US-08-764-100-13	Sequence 13, Appl
c 33	46.4	1.6	643	1	US-08-764-100-7	Sequence 7, Appl
c 34	46.4	1.6	2378	4	US-08-802-805D-20	Sequence 20, Appl
c 35	46.4	1.6	2993	1	US-08-764-100-2	Sequence 2, Appl
c 36	46.4	1.6	2993	1	US-08-764-100-10	Sequence 10, Appl
c 37	46.4	1.6	3000	1	US-08-764-100-9	Sequence 9, Appl
c 38	46.4	1.6	3001	1	US-08-764-100-1	Sequence 1, Appl
c 39	46.2	1.6	7859	1	US-07-854-596B-4	Sequence 4, Appl
c 40	46.2	1.6	7859	2	US-08-450-905B-15	Sequence 15, Appl
c 41	46.2	1.6	7859	3	US-07-982-759F-15	Sequence 15, Appl
c 42	46	1.6	1512	2	US-08-909-965C-8	Sequence 8, Appl
c 43	46	1.6	2435	4	US-09-306-593-1	Sequence 1, Appl
c 44	45.8	1.6	796	1	US-08-104-073-2	Sequence 2, Appl
c 45	45.8	1.6	1700	2	US-08-897-340-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-056-075-1
; Sequence 1, Application US/09056075
; Patent No. 5955368
; GENERAL INFORMATION:
; APPLICANT: Johnson, Eric A.
; APPLICANT: Bradshaw, Marite
; APPLICANT: Rood, Julian
; TITLE OF INVENTION: Expression System for Clostridium
; TITLE OF INVENTION: Species
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,075
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 3770..4013
; OTHER INFORMATION: /note= "RP4 origin of DNA transfer (orit) from
; OTHER INFORMATION: plasmid RP4"
US-09-056-075-1

Query Match 1.9%; Score 53; DB 2; Length 6243;
Best Local Similarity 49.5%; Pred. No. 0.00027;

	Matches	137;	Conservative	0;	Mismatches	140;	Indels	0;	Gaps	0;
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Db	1118	TATCTTTACAACCTCCCCAAAAAAGAAGTACAAAGTACCCTATAATACAAAGCGTA	1177							
Qy	2640	AAACAGCCTTAGTAAATTAACAACATTTTATACCAATAAAATTTTCAAAATATTACTAACTAA	2699							
Db	1178	AAAAANATGAGGTTAAATAAAAAAATAAAAAATAAAAAATAAAAAATAAAAAANAAT	1237							
Qy	2700	TGTAGCATTAACCTAACGATTGGAAACTACATTTTACAACCTTCAAAGCTGTGTTTTATACATAG	2759							
Db	1238	AAAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAA	1297							
Qy	2760	AAATCAATTACAGCTTTTAATTTGAAACCTGTAAACCATTTTGATTAATGCAACCAATATAAGCAT	2819							
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Qy	2820	CTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2856							
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RESULT 2
US-08-487-826B-13
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellemo, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92860
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-487-826B-13

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Best Local Similarity 51.8%; Pred. No.: 0.0033;

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Query Match          1.7%; Score 49.8; DB 3; Length 1776;
Best Local Similarity 66.1%; Pred. No. 0.001;
Matches 72; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 2748 TTTTATACATAGAAATCAATTACAGCTTTTAATTGAAACCTGTAACCATTTTGATATGCA 2807
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QY 2808 ACAATAAGCATCTTCCAAAAAAGATTTTAAATTTGAAACCTGTAACCATTTTGATATGCA 2856
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Db 1728 AAAAAAAGATTTTAAATTTGAAACCTGTAACCATTTTGATATGCA 1776

RESULT 4
US-09-258-016-10
; Sequence 10, Application US/09258016
; Patent No. 6362395
; GENERAL INFORMATION:
; APPLICANT: Bachettira W. Poovaiah, Zhihua Liu,
; APPLICANT: Shameekumar Patil, Daisuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,016
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephens Jr., Donald L.
; REGISTRATION NUMBER: 34,022
; REFERENCE/DOCKET NUMBER: 4630-51994
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1776 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; DESCRIPTION: Tobacco CCaMK cDNA and deduced amino-acid
; FEATURE:
; NAME/KEY: protein-coding sequence (not including
; NAME/KEY: stop codon)
; LOCATION: nucleotides 20-1570
US-09-258-016-10

Query Match          1.7%; Score 49.8; DB 4; Length 1776;
Best Local Similarity 66.1%; Pred. No. 0.001;
Matches 72; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 2748 TTTTATACATAGAAATCAATTACAGCTTTTAATTGAAACCTGTAACCATTTTGATATGCA 2807
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QY 2808 ACAATAAGCATCTTCCAAAAAAGATTTTAAATTTGAAACCTGTAACCATTTTGATATGCA 2856
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Db 1728 AAAAAAAGATTTTAAATTTGAAACCTGTAACCATTTTGATATGCA 1776

RESULT 5
US-09-257-825B-10
; Sequence 10, Application US/09257825B
; Patent No. 6403352
; GENERAL INFORMATION:
; APPLICANT: Poovaiah, Bachettira W.
; APPLICANT: Patil, Shameekumar
; APPLICANT: Takezawa, Daisuke
; TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
; FILE REFERENCE: 4630-51993
; CURRENT APPLICATION NUMBER: US/09/257,825B
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: US 08/655,352
; PRIOR FILING DATE: 1996-05-23
; PRIOR APPLICATION NUMBER: US 60/014,743
; PRIOR FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-257-825B-10

Query Match          1.7%; Score 49.8; DB 4; Length 1776;
Best Local Similarity 66.1%; Pred. No. 0.001;
Matches 72; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 2748 TTTTATACATAGAAATCAATTACAGCTTTTAATTGAAACCTGTAACCATTTTGATATGCA 2807
|||||
Db 1668 TTTTATCACTACTCGTAAAGATCCTTTTAATTAATTCGGAAGCCTTTATGTTAAAAA 1727

QY 2808 ACAATAAGCATCTTCCAAAAAAGATTTTAAATTTGAAACCTGTAACCATTTTGATATGCA 2856
|||||
Db 1728 AAAAAAAGATTTTAAATTTGAAACCTGTAACCATTTTGATATGCA 1776

RESULT 6
US-08-628-417-6
; Sequence 6, Application US/08628417
; Patent No. 5627054
; GENERAL INFORMATION:
; APPLICANT: GILLESPIE, DAVID
; TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
; ADDRESSEE: DEFENSE COMMAND
; STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
; CITY: ABERDEEN PROVING GROUND
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,417
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BIFFONI, ULYSSES J
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 398-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158

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; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligodeoxynucleotide
; HYPOTHEetical: NO
; ANTI-SENSE: YES
US-08-628-417-6

Query Match 1.7%; Score 49.4; DB 1; Length 240;
Best Local Similarity 51.6%; Pred. No. 0.00046;
Matches 113; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 2638 ACAACAGCCTTAGTAACTTAACATTTTATACCAATTAATTTTCAATATTTACTAACT 2697
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QY 2698 AATGTAGCATTAACACGATTGGAACATACATTTACAACTTCAAGCTGTTTATACAT 2757
Db 66 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 125

QY 2758 AGAAATCAATTACAGCTTTAATTTGAAACTGTAACTTTGATAATGCAACAATAAGC 2817
Db 126 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 185

QY 2818 ATCTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2856
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RESULT 7
US-07-861-458C-4
; Sequence 4, Application US/07861458C
; Patent No. 6232061
; GENERAL INFORMATION:
; APPLICANT: Marchionni, Mark Andrew
; APPLICANT: Johnson, Carl D.
; TITLE OF INVENTION: HOMOLOGY CLONING
; NUMBER OF SEQUENCES: 142
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/861.458C
; FILING DATE: 04/01/92
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1100
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-861-458C-4

Query Match 1.7%; Score 49.2; DB 4; Length 1100;
Best Local Similarity 73.3%; Pred. No. 0.0012;
Matches 63; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2771 AGCTTTAATGAAACTGTAAACCATTTTGATAATGCAACAATAAAGCATCTTCCAAAAA 2830
Db 997 ATCTCTAATGTATAGTAGCTTTTGTATTAATAAATAAATAAATAAATAAATAA 1056

QY 2831 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2856
Db 1057 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1082

RESULT 8
US-08-747-221B-24
; Sequence 24, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2836 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 99..1889
US-08-747-221B-24

Query Match 1.7%; Score 49; DB 3; Length 2836;
Best Local Similarity 58.6%; Pred. No. 0.0022;
Matches 85; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 2712 TAACGATTGAAACTACATTTTACAACTTTCAAGCTGTTTTATACATAGAAATCAATTACA 2771
Db 2688 TATGATTATATGTCAACATGTAAATACAAATCGGTGTTTAAATAATCTGTATTAAA 2747

QY 2772 GCTTTAATGAAACTGTAAACCATTTTGTATTAATGCAACAATAAAGCATCTTCCAAAAA 2831
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,677
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTSD:401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5173 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..4863
; US-08-242-677-1

Query Match 1.7%; Score 49; DB 1; Length 5173;
Best Local Similarity 69.1%; Pred. No. 0.0031;
Matches 67; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 2760 AAATCAATTACAGCTTTAAATTGAAACATGTAACCATTTTGATATATGCAACATAAAGCAT 2819
Db 5059 AATGTGATTTCTTCCTTTAATAAAATATTTTAAGCAATTTGTCCAATAAAAAAAAAAAAAA 5118

Qy 2820 CTTCCAAAAAIAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2856
Db 5119 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5155

RESULT 13
US-09-014-969-14
; Sequence 14, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,969
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284

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; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-014-969-14

Query Match
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Matches 118; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 2623 CTTACTATGAGCCTCAACAGCCTTAGTAATTAACCAATTTTACCAATTAATTTT 2682
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QY 2683 CAAATATTACTACTAATGTAGCAATTAACCTGGAACCTACATTACCACTTCAA 2742
Db 2274 AAAAAA 2333

QY 2743 AGCTGTTTATACATGAATCAATACAGCTTTAATGAAACTGTAACCAATTTTATA 2802
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QY 2803 ATGCAACAATAAGCATCTTCCAAAAA 2856
Db 2394 AAAAAA 2447

RESULT 14
US-08-924-747-25
; Sequence 25, Application US/08924747
; Patent No. 6063570
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: E.I. DU PONT DE NEMOURS AND COMPANY
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,747
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CL-1108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 991 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

; ORIGINAL SOURCE:
; TISSUE TYPE: SOYBEAN
; IMMEDIATE SOURCE:
; CLONE: SSM.PK0067.G5
; US-08-924-747-25

Query Match
Best Local Similarity 1.7%; Score 48.2; DB 3; Length 991;
Matches 65; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Db 891 CTATTTTAAATTTTAACTAAATAAAGTGTTTCAGTTTAAAAA 950

QY 2824 CAAAAA 2856
Db 951 AAAAAA 983

RESULT 15
US-09-247-373B-25
; Sequence 25, Application US/09247373B
; Patent No. 6168954
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1108-A
; CURRENT APPLICATION NUMBER: US/09/247,373B
; CURRENT FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 08/924,747
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; TYPE: DNA
; ORGANISM: SOYBEAN
; US-09-247-373B-25

Query Match
Best Local Similarity 1.7%; Score 48.2; DB 4; Length 991;
Matches 65; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2764 CAATTACAGCTTTAATTTGAAACTGTAAACCAATTTTGTATGATAATGCAACAATAAAGCATCTTC 2823
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QY 2824 CAAAAA 2856
Db 951 AAAAAA 983

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GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 22:36:08 ; Search time 577.385 Seconds
(without alignments)
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Title: US-09-778-971-2

Perfect score: 2856

Sequence: 1 cggcgatcgtcgtcgtg.....aaaaaaaaaaaaaaaaaaaaa 2856

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IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2855	100.0	2856	22 AAD13444	Human interleukin-
2	2652	92.9	2725	24 ABL61567	Human interleukin
C 3	1178.8	41.3	32177	22 ABA18493	Human nervous syst
C 4	1178.8	41.3	32177	22 AAS29828	Human cytoskeletal
C 5	1178.8	41.3	32177	22 AAL05374	Human reproductive
6	1078	37.7	1827	22 AAD13443	Human interleukin-
7	1051.2	36.8	1701	21 AAA87757	Human secreted pro
8	1051.2	36.8	1701	21 AAF64039	cDNA encoding huma
9	1041.8	36.5	1796	22 AAS18126	Human DNAX cytokin

10	1040.2	36.4	1713	24 ABA03202	Human IL-17 recept
11	1040.2	36.4	1841	24 AAD28776	Human interleukin-
12	1040.2	36.4	1841	24 ABA03200	Human IL-17 recept
13	1040.2	36.4	2015	24 AAD28777	Human interleukin-
14	1040.2	36.4	2015	24 ABA03201	Human IL-17 recept
15	1039.6	36.4	2161	22 AAH99008	Human EST-derived
16	1038.6	36.4	1818	22 AAD12581	Human protein havi
17	1038.6	36.4	1918	21 AAA75772	cDNA encoding a hu
18	1038.6	36.4	1918	21 AAZ52046	cDNA encoding inte
19	1031.4	36.1	1816	21 AAA75761	cDNA encoding a hu
20	1031.4	36.1	1816	21 AAZ52035	cDNA encoding inte
21	1031.4	36.1	1816	21 AAZ52035	Human interleukin
22	936.6	32.8	2080	21 AAA95789	Human immune syate
23	763.4	26.7	1515	22 AAS46124	Human DNA encoding
24	763.4	26.7	1515	22 AAS09514	Human CDNA encoding
25	763.4	26.7	1515	22 AAF92136	Human PRO5801 cDNA
26	559.4	19.6	714	20 AAZ08982	Human IL-17RH cDNA
27	551	19.3	1506	24 AAS18127	Human DCRS6 revers
28	498.6	17.5	1963	22 AAD13445	Mouse interleukin-
29	498.6	17.5	2589	22 AAD13446	Mouse interleukin-
C 30	451	15.8	603	24 ABQ59113	Human colon cancer
C 31	353.2	12.4	471	24 ABQ58257	Human colon cancer
32	331.6	11.6	405	22 AAF66413	Novel human polynu
33	329.8	11.5	397	22 AAF66470	Novel human polynu
34	326.4	11.4	409	21 AAA75762	cDNA clone sequenc
35	326.4	11.4	409	21 AAZ52036	HPCH63R cDNA clon
36	326.4	11.4	409	21 AAZ35747	Human interleukin
37	242.4	8.5	374	22 AAF98686	Human ovarian canc
38	205.4	7.2	218	16 AAT24669	Human gene signatu
39	182.6	6.4	327	21 AAF75763	cDNA clone sequenc
40	182.6	6.4	327	21 AAZ52037	HETCC45RA cDNA clo
41	182.6	6.4	327	21 AAZ35748	Human interleukin
42	139.4	4.9	637	24 AAS18128	Mouse DNAX cytokin
C 43	114	4.0	116	19 AAX12137	Human biallelic po
44	108.8	3.8	210	24 AAS18129	Mouse DCRS6 revers
C 45	65	2.3	6694	24 ABL70352	Chemically treated

ALIGNMENTS

RESULT 1
AAD13444

ID AAD13444 standard; cDNA; 2856 BP.

AC AAD13444;

XX AAD13444;

XX AAD13444;

DT 06-NOV-2001 (first entry)

XX Human interleukin-17 receptor related protein (Evi27) encoding cDNA #2.

DE Human; interleukin-17 receptor related protein; IL-17; chromosome 3p21;

XX Evi27; retroviral integration; chromosomal mapping; mutational analysis;

KW BXH2 murine myeloid leukaemia; proinflammatory cytokine; IL-8; therapy;

KW haematopoietic cell; cancer; autoimmune disease; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

QY 1741 ATGCATGGTGTGAACCTTCTGAGCCTCTGTTTCTCAGCTGACTCCATATTTTCCTA 1800
Db 1741 ATGCATGGTGTGAACCTTCTGAGCCTCTGTTTCTCAGCTGACTCCATATTTTCCTA 1800
QY 1801 CTTGTGGCAGCAGCTCATCCGACATAAAGGAACAGTGTGCTCTGCCACAAACAGGCG 1860
Db 1801 CTTGTGGCAGCAGCTCATCCGACATAAAGGAACAGTGTGCTCTGCCACAAACAGGCG 1860
QY 1861 TCCCTTTCCCTCTGGATAACAAAGCAAGCGGAGGCTGGCTCTCTCTCTGC 1920
Db 1861 TCCCTTTCCCTCTGGATAACAAAGCAAGCGGAGGCTGGCTCTCTCTCTGC 1920
QY 1921 TGTCTCTGCTGGGCAATGAGGCTGTGGCAGGATCTATCTAATGTGGAGCAG 1980
Db 1921 TGTCTCTGCTGGGCAATGAGGCTGTGGCAGGATCTATCTAATGTGGAGCAG 1980
QY 1981 AAAGGATCAAGAGACTCTCTTTTACCAACACACTACTGCCCCCAATTAAGTCTTG 2040
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Db 2041 TGGTTTACCCTATCTGAATATGTTTCCATCACAAATTTGTTACTTCACTGAATTTCTTC 2100
QY 2101 AAAACATTGCAAGAGTGGTCTATCCTTGAAGTGGCAGAAAAAGAAATAGCAGAGA 2160
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QY 2161 TGGGTCAGTGGAGTGGCTGCTCACTCAAAAGAGCAGCAGCAAGTCTCTCTTC 2220
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QY 2281 GTGAGAACTCTCAAGACCTTCTCCCTGCTTAACTTTTCTGAGTGTCTAAGAA 2340
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QY 2401 ATTACATGCTCTCAGTGTCTGCCCAAGTACCCTTTCTAAGAGTGTCTTCTTCT 2460
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QY 2461 GTGCAAACTTCTTCAATGTCAAGCAGCAGTGTGTCAGAGGAAAGATCACAAGCCTGCC 2520
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QY 2521 ACGATGGCTGTGCTCTTGTAGCCACCCATGAGAGCAAGAGCTTAAAGGCTTCT 2580
Db 2521 ACGATGGCTGTGCTCTTGTAGCCACCCATGAGAGCAAGAGCTTAAAGGCTTCT 2580
QY 2581 ATCCCAACCAATTACAGGAAACAACTGTGTATGATCTCTGAGCTTACTATGAGCCTTCA 2640
Db 2581 ATCCCAACCAATTACAGGAAACAACTGTGTATGATCTCTGAGCTTACTATGAGCCTTCA 2640
QY 2641 AACAGCCTTTAGTAATTAACCAATTTTATACCAATAAAATTTTCAATATTTACTAATA 2700
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QY 2701 GTAGCAATTAACCAATTGGAACCTATCAATTTACATCTCAAGCTGTTTTATACATAGA 2760
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QY 2761 AATCAATTAACAGCTTTAATTTGAACCTGTAAACCTTTTATGATGCAACAAATGAACATC 2820
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QY 2821 TTCCAAAAA 2856
Db 2821 TTCCAAAAA 2856
RESULT 2
ID ABL61567 standard; cDNA; 2725 BP.
AC ABL61567;
XX
DT 20-SEP-2002 (first entry)
XX
DE Human interleukin receptor-ligand (IL-17B and IL17BR) 32.56 cDNA.
XX
KW Human; interleukin receptor-ligand (IL-17B and IL17BR) 32.56;
KW rheumatoid arthritis; inflammation; immunological disease; tumour;
KW development disturbance; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1689..2579
FT /*tag= a
FT /product= "interleukin receptor-ligand (IL-17B and
IL17BR) 32.56"
XX
PN CN1341660-A.
XX
PD 27-MAR-2002.
XX
PF 07-SEP-2000; 2000CN-0125085.
XX
PR 07-SEP-2000; 2000CN-0125085.
XX
PA (SHAN-) SHANGHAI BIODOR GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-520727/56.
XX
PS P-PSDB; ABB84242.
XX
PT Novel human interleukin receptor-ligand (IL-17B and IL17BR) 32.56 -
XX
PS Claim 6; Page 25-26 (Disclosure); 33pp; Chinese.
XX
CC This invention describes a novel human interleukin receptor-ligand
CC (IL-17B and IL17BR) 32.56. The product of the invention can be used to
CC treat several diseases, such as rheumatoid arthritis, inflammation,
CC immunological disease, various tumours and development disturbance. This
CC sequence encodes the human interleukin receptor-ligand (IL-17B and
CC IL17BR) 32.56 described in the method of the invention.
XX
SQ Sequence 2725 BP; 705 A; 649 C; 686 G; 685 T; 0 other;
Query Match 92.9%; Score 2652; DB 24; Length 2725;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2672; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
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Db 38 CGCGCATGCTGCTGCTGCTGATGAAGCTGGCGCGCTGTGAGGAGCGCGTACCCCGAG 97
QY 61 AGCCGACCGTTCATATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGTACACATG 120
Db 98 AGCCGACCGTTCATATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGTACACATG 157
QY 121 ATCTAATCCCGGAGACTTTGAGGAGCTCCGAGTAGAACCTTTCAACTAGTTTGCAA 180
Db 158 ATCTAATCCCGGAGACTTTGAGGAGCTCCGAGTAGAACCTTTCAACTAGTTTGCAA 217
QY 181 CAGGGGACTTATCAATTTTGTATGATGTAAGCTGGGTACTCCGGGAGATGCCAGATCC 240

Db 218 CAGGGGACTATTCAATTTTGATGAATGAAGCTGGGTATCTCCGGGCGAGATGCCAGCATCC 277
QY 241 GCTTGTGAAGGCGCACCAAGATTGTGTGACGGGCAAAAGCAACTTCCAGTCTCTACAGCT 300
Db 278 GCTTGTGAAGGCGCACCAAGATTGTGTGACGGGCAAAAGCAACTTCCAGTCTCTACAGCT 337
QY 301 GTGTAGGTCGAATTAACACAGAGGCGCTTCCAGACTCAGACCAAGCCCTCTGGTGGTAAAT 360
Db 338 GTGTAGGTCGAATTAACACAGAGGCGCTTCCAGACTCAGACCAAGCCCTCTGGTGGTAAAT 397
QY 361 GGACATTTTCTATATCCGCTTCCGTGTAGAGCTGAACACAGCTCTATTTCATTTGGGGCCC 420
Db 398 GGACATTTTCTATATCCGCTTCCGTGTAGAGCTGAACACAGCTCTATTTCATTTGGGGCCC 457
QY 421 ATAAATATTCCTAATGCAAAATGAATGAAGATGGCCCTTCCATGTCTGTGAAATTCACCT 480
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QY 541 TGTGGATCCGAACATCACTGCTTGTGAAGAGAAATGAGGAGACAGTAGAAGTGAATTCAC 600
Db 578 TGTGGATCCGAACATCACTGCTTGTGAAGAGAAATGAGGAGACAGTAGAAGTGAATTCAC 637
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Db 638 CAACCACTCCCTCGGGAACAGATACATGCTCTTATCCAAACAGACACTATCATCGGGT 697
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QY 841 CAAATGCATCTTCCAGACAGACACCAAGTTAAGTGCCTTCATGGGGGTTCTTCGCTGC 900
Db 878 CAAATGCATCTTCCAGACAGACACCAAGTTAAGTGCCTTCATGGGGGTTCTTCGCTGC 937
QY 901 AGCCTCCAGCTGCTGAGTGCAGAGCGGACGTCGAGTTGGTCCCTTTGCTTGT 960
Db 938 AGCCTCCAGCTGCTGAGTGCAGAGCGGACGTCGAGTTGGTCCCTTTGCTTGT 997
QY 961 TTAATGGCTGCTGACCTTCCAAAGCACTTTTATTTTCAATTTTCTCTCAGACACTCAG 1020
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QY 1261 GGGGACACAGCCACTCCCAAGAAATGAAGAACTTCCATGCTTCAATCCCTGGCATAAA 1320
Db 1298 -GGGACACAGCCACTCCCAAGAGTAAGAGCTTCCATGCTTCAATCCCTGGCATAAA 1356

QY 1321 AGTGNTCAAACACACACAGAGGGGCGAGGCAACAGCCAGGCTATGATGGGTACTACCTTT 1380
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QY 1381 TCTGGAAACCAATAGACTTTCCTTACTACAGGACTTGTGATGCTCTAAAGCACTGGCTGA 1440
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QY 2341 GGCAGATTCATCTGCACAAATACGTGGTGTCTACTTTAGAGAGATTTGATACAAAGAGCG 2400
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Db	2437	ATTACATGCTCTCAGTGTCTGCCCCAGTACCACTTCATGAAGGATGCCACTGCTTTCT	2496	PR	14-AUG-2000;	2000US-0225757.
QY	2461	GTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAAGGAAAAAGATCAACAAGCTTGCC	2520	PR	18-AUG-2000;	2000US-0226279.
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QY	2521	ACGATGGCTGCTCTCTTGTAGCCCAACCCATGAGAGACCTTAAAGGCTTTCCT	2580	PR	22-AUG-2000;	2000US-0226868.
Db	2557	ACGATGGTGTCTCTCTTGTAGCCCAACCCATGAGAGACCTTAAAGGCTTTCCT	2616	PR	23-AUG-2000;	2000US-0227182.
QY	2581	ATCCCAACCAATTACAGGAAAAACGTGTGATCTCTGAGCTTACTATGCAGCCTACA	2640	PR	30-AUG-2000;	2000US-0227009.
Db	2617	ATCCCAACCAATTACAGGAAAAACGTGTGATCTCTGAGCTTACTATGCAGCCTACA	2676	PR	01-SEP-2000;	2000US-0228924.
QY	2641	AACAGCCTTAGTAAATTAACAATTTTATACCAATAAAATTTTCAAAATAT	2689	PR	01-SEP-2000;	2000US-0229287.
Db	2677	AACAGCCTTAGTAAATTAACAATTTTATACCAATAAAATTTTCAAAATAT	2725	PR	01-SEP-2000;	2000US-0229343.

RESULT 3
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 ID ABA18493 standard; DNA; 32177 BP.
 XX ABA18493;
 AC ABA18493;
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Human nervous system related polynucleotide SEQ ID NO 10824.
 XX
 KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
 KW antiparkinsonian; antisickling; antianemic; antithratic; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200159063-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01334.
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 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0203515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
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 PR 14-AUG-2000; 2000US-0225266.
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08-NOV-2000; 2000US-0246532.
 08-NOV-2000; 2000US-0246609.
 08-NOV-2000; 2000US-0246610.
 08-NOV-2000; 2000US-0246611.
 08-NOV-2000; 2000US-0246613.
 17-NOV-2000; 2000US-0249207.
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 17-NOV-2000; 2000US-0249216.
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 17-NOV-2000; 2000US-0249244.
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 17-NOV-2000; 2000US-0249264.
 17-NOV-2000; 2000US-0249265.
 17-NOV-2000; 2000US-0249297.
 17-NOV-2000; 2000US-0249299.
 17-NOV-2000; 2000US-0249300.
 01-DEC-2000; 2000US-0250391.
 01-DEC-2000; 2000US-0251160.
 05-DEC-2000; 2000US-0251030.
 05-DEC-2000; 2000US-0251988.
 05-DEC-2000; 2000US-0256719.
 06-DEC-2000; 2000US-0251479.
 08-DEC-2000; 2000US-0251856.
 08-DEC-2000; 2000US-0251869.
 08-DEC-2000; 2000US-0251989.
 08-DEC-2000; 2000US-0251990.
 11-DEC-2000; 2000US-0254097.
 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-541565/60.
 Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 useful for preventing, diagnosing and/or treating nervous system
 cancers and metastases -
 Disclosure; SEQ ID NO 10824; 1701pp + Sequence Listing; English.
 The invention relates to novel genes (AB11004-AB21534) and proteins
 (AB114678-AB18001) useful for preventing, treating or ameliorating
 medical conditions e.g. by protein or gene therapy. The genes are
 isolated from a range of human tissues disclosed in the specification.
 The nucleic acids, proteins, antibodies and (ant)agonists are useful
 in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 and ovarian cancer and other cancers of the adrenal gland, bone, bone
 marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 and parasitic infections.
 Note: The sequence data for this patent did not form part of the
 printed specification, but was obtained in electronic format directly
 from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 Sequence 32177 BP; 8826 A; 6801 C; 7130 G; 9420 T; 0 other;

Query Match 41.3%; Score 1178.8; DB 22; Length 32177;
 Best Local Similarity 98.0%; Pred. No. 4.7e-269;

	Matches 1203;	Conservative 0;	Mismatches 23;	Indels 1;	Gaps 1;			
QY 663	TCTCAGGTGTTT	GAGCACA	CACAGAA	CAAAACG	CAGCTT	CAGTGTGAT	TCCAGTG	722
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QY 723	ACTGGGATAGT	GAAGTGT	CTACGGT	GCAGG	TAAAGT	TCAGT	AGCTCT	782
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QY 783	AGGGACATAG	AAGACTG	TTCATCA	TTCCTTT	TAAGAT	GATGAT	TCTCTGTCA	842
DB 24432	AGGGACATAG	AAGACTG	TTCATCA	TTCCTTT	TAAGAT	GATGAT	TCTCTGTCA	24373
QY 843	AATGCATCTT	CGCAGCA	CACACAG	CTTAA	GGGGT	TCATGGG	GTCTT	902
DB 24372	AATGCATCTT	CGCAGCA	CACACAG	CTTAA	GGGGT	TCATGGG	GTCTT	24313
QY 903	CCTCCACCGT	GTGAGGT	CCAGG	CCGAC	GTGG	CAGTGT	CGTCC	962
DB 24312	CCTCCACCGT	GTGAGGT	CCAGG	CCGAC	GTGG	CAGTGT	CGTCC	24253
QY 963	AATGGCTGCT	GACCTTC	CAAAG	CACCTTT	TATTT	TCATTT	CTGTCA	1022
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DB 24192	ATAGCAGTAC	CAATTTT	ACTTCC	GCAAG	CTTAA	CTGCA	AGCTG	24133
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QY 1143	CTCTGGGCG	AGCGG	CCAGC	CTG	GAAC	AGAGTT	GGAG	1202
DB 24072	CTCTGGGCG	AGCGG	CCAGC	CTG	GAAC	AGAGTT	GGAG	24013
QY 1203	CTCTCAGTAT	GTCTCTT	TCAACT	CTAGT	TTT	TTT	TTT	1262
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DB 23953	GGACACAGCC	ACTCCCA	AAAGAT	TAAG	AACTT	CCATCT	CCCTG	23894
QY 1323	TGNTCAAC	CACACAG	AGGGG	CCAGC	ACC	AGG	GTATG	1382
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DB 23833	TGGAGAAC	CATAGAC	TCCCTT	TACT	ACAGG	GAATG	GCATG	23774
QY 1443	GAAGCCAA	GAGGAT	CAC	TGCTCT	CTCTCT	TTTTT	TGTAG	1502
DB 23773	GAAGCCAA	GAGGAT	CAC	TGCTCT	CTCTCT	TTTTT	TGTAG	23714
QY 1503	GATATGAC	CTAGCC	CTTTT	AGT	TAAG	CAAG	CTG	1562
DB 23713	GATATGAC	CTAGCC	CTTTT	AGT	TAAG	CAAG	CTG	23654
QY 1563	GGTTCCAG	ACCCG	GAGTCT	TGGG	CACTG	GGGT	CTC	1622
DB 23653	GGTTCCAG	ACCCG	GAGTCT	TGGG	CACTG	GGGT	CTC	23594
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DB 23593	CTTTGTTA	CAGATGT	GTG	ACCA	AGGGG	AAAAAT	GTGCAT	23534
QY 1693	AGCCAGAA	GAGGAA	GTGTT	TGG	CTC	AGT	AGG	1742
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OY 1803 TGTGGCAGCGACTGCTCCGACATGAAGCAAGTGTCTCTGCCCAACAAAGCGGTC 1862
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DB 23413 TGTGGCAGCGACTGCTCCGACATGAAGCAAGTGTCTCTGCCCAACAAAGCGGTC 23354
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OY 1863 CCTTCCCTCTGGATAACAAACAAAGC 1889
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DB 23353 CCTTCCCTCTGGATAACAAAGTGC 23327
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RESULT 4
ID AAS29828 standard; DNA; 32177 BP.
XX
AC AAS29828;
XX
XX
DT 21-NOV-2001 (first entry)
XX
DE Human cytoskeletal element-related polypeptide encoding genomic DNA #15.
XX
KW Cytoskeletal element-related protein; human; mouse; rabbit; goat; horse;
KW cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective;
KW cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
KW ophthalmological; vulnary; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; db;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; endocrine infection;
KW gastrointestinal disorder; renal disorder; respiratory disorder;
KW wound healing; skin aging; organ transplantation; food preservative;
KW tissue regeneration; anti-infertility; food additive.
XX
OS Homo sapiens.
XX
FN WO200155168-A1.
XX
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01331.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
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PR 14-AUG-2000; 2000US-0224519.
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PR 23-AUG-2000; 2000US-0227009.
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PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
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PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
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PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
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PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.


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QY 1863 CTTTCCCTCTCGATAACAACAAAAGC 1889
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RESULT 5
ID AAL05374/c
ID AAL05374 standard; DNA; 32177 BP.
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AC AAL05374;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 8062.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; Gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01339.
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PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
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PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
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BXH2 murine myeloid leukaemia; proinflammatory cytokine; IL-8; therapy;
haematopoietic cell; cancer; autoimmune disease; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 6..1514

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FT /product= "Human Evi27 protein"

FT sig_peptide 6..44

FT /*tag= b

FT mat_peptide 45..1511

FT /*tag= c

FT /product= "Human mature Evi27 protein"

XX WO200157202-A2.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US03518.

XX 04-FEB-2000; 2000US-0180374.

XX (UYAR-) UNIV ARKANSAS.

XX Shaughnessy JD;

XX WPI; 2001-496920/54.

XX P-PSDB; AAE07160.

XX New nucleic acids encoding an interleukin (IL)-17 receptor related
protein for use as a marker for leukemia
Claim 1a; Page 74-75; 87pp; English.

CC The present sequence is a cDNA encoding human interleukin (IL)-17
receptor related protein (Evi27). Human Evi27 gene was mapped to
chromosome 3p21. Evi27 is a common site of retroviral integration
in BXH2 murine myeloid leukaemias. Evi27 cDNA sequences are useful
as antisense molecules to inhibit Evi27 protein or for chromosomal
mapping or mutational analysis of Evi27 protein. They are proviral
integration sites associated with leukaemias and monitoring this
site provides a genetic tag for disease gene identification. The
proteins of the invention are useful to stimulate the secretion of
proinflammatory cytokines such as IL-8 and plays an important role
in the developmental and/or disease processes of haematopoietic
cells. Hence modulating the expression of Evi27 at the RNA or
protein level is used in the treatment of diseases such as cancer
or autoimmune diseases.

XX Sequence 1827 BP; 547 A; 438 C; 397 G; 445 T; 0 other;

XX Query Match 37.7%; Score 1078; DB 22; Length 1827;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-245;

XX Matches 1078; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1779 CAGCTGACCTCCATATTTCTTCTGTCGAGCGCTCGATCGACATAAAGGACAGTT 1838

DB 750 CAGCTGACCTCCATATTTCTTCTGTCGAGCGCTCGATCGACATAAAGGACAGTT 809

QY 1839 GTGCTGTGCCCAACAACAGCGCTCCCTTTCCCTGTGGATAACAACAAAGCAGCGGA 1898

DB 810 GTGCTGTGCCCAACAACAGCGCTCCCTTTCCCTGTGGATAACAACAAAGCAGCGGA 869

QY 1899 GCGTGGCTGCTCTCTCTGCTGTCTCTGCTGTGGCCACATGGGTGTGGTGGCAGGG 1958

DB 870 GCGTGGCTGCTCTCTCTGCTGTCTCTGCTGTGGCCACATGGGTGTGGTGGCAGGG 929

QY 1959 ATCTATCTAATGTGGAGGACCAAGGATCAAGAGACTTCTTTTCTTACCACCACTA 2018

DB 930 ATCTATCTAATGTGGAGGACCAAGGATCAAGAGACTTCTTTTCTTACCACCACTA 989

QY 2019 CTGCCCCCATTAAGTCTTCTGTGGTTTACCCTCTGAAATATGTTTCCATCACAAT 2078

DB 990 CTGCCCCCATTAAGTCTTCTGTGGTTTACCCTCTGAAATATGTTTCCATCACAAT 1049

QY 2079 TGTACTTCACTGAATTTCTTCAAAACCAATTGCAGAGTGAAGTCACTCTTCAAAAGTGG 2138

DB 1050 TGTACTTCACTGAATTTCTTCAAAACCAATTGCAGAGTGAAGTCACTCTTCAAAAGTGG 1109

QY 2139 CAGAAAAGAAAATAGCAGAGATGGTCCAGTGCAGTGGCTTGCCTGCCACTCAAAAGAGGCA 2198

DB 1110 CAGAAAAGAAAATAGCAGAGATGGTCCAGTGCAGTGGCTTGCCTGCCACTCAAAAGAGGCA 1169

QY 2199 GCAGACAAAGTCTCTCTTCTTCCATGACGCTCAACAGTGTGTGGCATGGTACCTCT 2258

DB 1170 GCAGACAAAGTCTCTCTTCTTCCATGACGCTCAACAGTGTGTGGCATGGTACCTCT 1229

QY 2259 GCGAAGAGCGAGGCGAGTCCAGTGAAGACTCTCAAGAGCTCTTCCCTCTTGCCTTTAAC 2318

DB 1230 GCGAAGAGCGAGGCGAGTCCAGTGAAGACTCTCAAGAGCTCTTCCCTCTTGCCTTTAAC 1289

QY 2319 CTTTTCTGCAGTGATCTAAGAACCCAGATTCAATGCTCTGACAAATAGCTGTGTCTACTTT 2378

DB 1290 CTTTTCTGCAGTGATCTAAGAACCCAGATTCAATGCTCTGACAAATAGCTGTGTCTACTTT 1349

QY 2379 AGAGAGATTGATACAAAAGACGATTCAATGCTCTGACAAATAGCTGTGTCTACTTT 2438

DB 1350 AGAGAGATTGATACAAAAGACGATTCAATGCTCTGACAAATAGCTGTGTCTACTTT 1409

QY 2439 ATGAAGAGTGCACCTGCTTCTTCTGTCAGAACTTCTCCATGTCAAGCAGCAGGTGTGAGCA 2498

DB 1410 ATGAAGAGTGCACCTGCTTCTTCTGTCAGAACTTCTCCATGTCAAGCAGCAGGTGTGAGCA 1469

QY 2499 GGAAGAAAGATCAAGAGCTGCCAGATGGCTGCTGCTCTTGTAGCCCACTGAGAAAG 2558

DB 1470 GGAAGAAAGATCAAGAGCTGCCAGATGGCTGCTGCTCTTGTAGCCCACTGAGAAAG 1529

QY 2559 CAAAGAGACCTTAAAGGCTTCTTATCCCAATTAACAGGGAAGAAACGTTGATGATCTT 2618

DB 1530 CAAAGAGACCTTAAAGGCTTCTTATCCCAATTAACAGGGAAGAAACGTTGATGATCTT 1589

QY 2619 GAAGCTTACTATGTCAGCTTACAAACAGCTTAGTAAATTAACCAATTTATACCAATAAAA 2678

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DB 1710 TCAAGAGCTGTTTATACATAGAAATCAATTAACGCTTTTAAATTAACCAATTTT 1769

QY 2799 GATAATGCAACAATAAAGCATCTTCCAAAAAAGAAAAAAGAAAAAAGAAAAA 2856

DB 1770 GATAATGCAACAATAAAGCATCTTCCAAAAAAGAAAAAAGAAAAAAGAAAAA 1827

RESULT 7

AAA87757

ID AAA87757 standard; cDNA; 1701 BP.

XX AC AAA87757;

XX AC AAA87757;

XX AC AAA87757;

XX AC AAA87757;

XX AC AAA87757;

DE Human secreted protein encoding cDNA SEQ ID #56.

KW Human; secreted protein; forensic procedure; gene therapy;
KW Chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;
KW Cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
KW Brain disorder; skeletal muscle disorder; eye disorder; obesity;
KW Mitochondriopathy; diabetes; atherosclerosis; Alzheimer's disease;
KW Neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
KW Septic shock; impotence; ss.

Dd 1626 TCAAGCTGTTTTATACATAGAATACTAATTACAGCTTTAATTGA AAAACTGTAAACCATT TT 1685

Qy 2799 GATAATGCAACAATAAAGCATCTTC 2823
|||||
Dd 1686 GATAATGCAACAATAAAGCATCTTC 1710
|||||

RESULT 11
AAD28776
ID AAD28776 standard; DNA; 1841 BP.
XX AC AAD28776;
XX DT 07-MAY-2002 (first entry)
XX XX Human Interleukin-17 receptor B-2 (IL-17RB-2) DNA.
DE DE
DE DE
KW KW Human; interleukin-17 receptor B-2; IL-17RB-2; immune system dysfunction;
KW KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;
KW KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;
KW KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;
KW KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;
KW KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;
KW KW ezema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;
KW KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;
KW KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;
KW KW cancer; diabetes; ds.
XX XX
OS OS Homo sapiens.
XX XX

Key Location/Qualifiers
CDS 50..1558
FT FT /*tag= a
FT FT /product= "Human IL-17RB-2 protein"
FT FT 50..92
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FT FT 93..1555
FT FT /*tag= c
FT FT /product= "Mature IL-17RB-2 protein"
XX XX
XX W0200208285-A2.
XX XX
PD PD 31-JAN-2002.
XX XX
PF PF 21-JUN-2001; 2001WO-US19861.
XX XX
PR PR 22-JUN-2000; 2000US-213125P.
PR PR 02-FEB-2001; 2001US-286159P.
PR PR 16-MAR-2001; 2001US-0810384.
XX XX
PA PA (AMGE-) AMGEN INC.
XX XX
PI PI Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;
DR DR WPI; 2002-155217/20.
DR DR P-PSDB; AAEE18127.
XX XX
PT PT Nucleic acid molecules encoding Interleukin 17 (IL-17) - like
PT PT polypeptides useful in the treatment, prevention and diagnosis of
PT PT diseases e.g. cancer
XX XX
XX Disclosure; Page 230-232; 242pp; English.

CC CC The invention relates to nucleic acid molecules encoding Interleukin 17
CC CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels
CC CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,
CC CC preventing or ameliorating a disease, such as immune system dysfunction
CC CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease);
CC CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel
CC CC disease, transplant rejection, graft vs. host disease); infections (HIV,
CC CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,
CC CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung
CC CC acute respiratory distress syndrome, cystic fibrosis, emphysema); skin

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 22:37:09 ; Search time 7273.44 Seconds
(without alignments)
11427.544 Million cell updates/sec

Title: US-09-778-971-2

Perfect score: 2856

Sequence: 1 cggcgatgcctgctgtg.....aaaaaaaaaaaaaaaaaaaaa 2856

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											</
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ALIGNMENTS

RESULT 1
AF208111

LOCUS

AF208111 Homo sapiens truncated IL-17 receptor homolog precursor (EVI27)
2856 bp mRNA linear PRI 17-JUL-2000

DEFINITION

AF208111 mRNA, complete cds.

ACCESSION

AF208111 GI:9246434

VERSION

AF208111

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 2856)

AUTHORS

Tian, E., Sawyer, J.R., Largaespada, D.A., Jenkins, N.A., Copeland, N.G. and Shaughnessy, J.D. Jr.

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

TITLE Evi27 encodes a novel membrane protein with homology to the IL17 receptor

JOURNAL Oncogene 19 (17), 2098-2109 (2000)

MEDLINE 20273223

PUBMED 10815801

REFERENCE 2 (bases 1 to 2856)

AUTHORS Shaughnessy, J.D. Jr.

TITLE Direct Submission

JOURNAL Submitted (24-NOV-1999) Myeloma and Transplantation Research Center, University of Arkansas for Medical Sciences, 4301 W. Markham St., Little Rock, AR 72212, USA

FEATURES

source Location/Qualifiers

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="3"

/map="3p21"

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/note="linked to ecotropic viral integration site 27 in murine myeloid leukemias"

CDS 6..872

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/note="lacks transmembrane and cytoplasmic domains"

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mat_peptide 45..869

/gene="EVI27"

misc_feature 204..206

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/note="truncated IL-17 receptor homolog"

misc_feature 312..314

/note="putative; glycosylation site"

misc_feature 471..476

/gene="EVI27"

/note="putative; glycosylation site"

misc_feature 480..482

/gene="EVI27"

/note="putative; glycosylation site"

misc_feature 594..596

/gene="EVI27"

/note="putative GSK3; phosphorylation site"

misc_feature 753..1784

/gene="EVI27"

/note="putative; glycosylation site"

polya_signal 2672..2677

/note="unspliced intron in this isoform"

BASE COUNT 793 a 655 c 682 g 725 t 1 others

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AGCCGACCGCTTCATGTGCTCTGAACACTGGGCCATCTCCAGAGTGGATGCTACACATG 120

QY 121 ATCTAATCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTCTTACAACTAGTGTGCAA 180

DB 121 ATCTAATCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTCTTACAACTAGTGTGCAA 180

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DB 181 CAGGGAGCATTTCAATTTTGTATGAATGTAAGCTGGGTACTCCGGGAGATGCCAGCATCC 240

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DB 241 GCTTGTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTTACAGCT 300

QY 301 GTGTGAGGTGCAATTTACACAGAGGCTTCCAGACTCAGACAGACCCCTCTGTGGTGAAT 360

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QY 601 CAACCACTCCCTCGGAACAGATACATGGCTCTTATCCACACAGCACTATCATCGGT 660

DB 601 CAACCACTCCCTCGGAACAGATACATGGCTCTTATCCACACAGCACTATCATCGGT 660

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DB 721 TGACTGGGATAGTAGAAGGTGCTACGGTGCAGGTAAAGTTTAAAGTATGATGCTCTCTGGGAG 780

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DB 781 GGAAGGACATAGAGACTGTTCCATCATTCATTCCTTTTAAAGTATGATGCTCTCTCTGT 840

QY 841 CAAATGCACTTCTGCCAGACACACAGTAAAGTGGCGCTTCATGGGGGTTCCTTCGCTGC 900

DB 841 CAAATGCACTTCTGCCAGACACACAGTAAAGTGGCGCTTCATGGGGGTTCCTTCGCTGC 900

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DB 901 AGCTTCCACCGTGTGAGGTGAGAGCCGACGTCGAGTGTGTGGTCCCTTTTGTGTTGTA 960

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DB 1081 TTGAAATGGGAAGGTTTGAAGTTCAGGAGCCGATGAACCTCTGGAGAGGGGCTGCCAGTC 1140

QY 1141 CTCTCTGGGCGCAGCGGACCCAGCTGGAAACACAGGAGTTGGAGCAGTAGTGTCTCTT 1200

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RESULT 2 AC113172/c

LOCUS AC113172 149634 bp DNA linear PRI 31-JUL-2002
 DEFINITION Homo sapiens chromosome 3 clone RP11-739J4, complete sequence.
 ACCESSION AC113172
 VERSION AC113172.2 GI:22024573
 KEYWORDS HTG.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 149634)
 Kaul, R. K., Olson, M. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z.,
 Saenphimmachak, C., Phelps, K. A., Buckley, D., Kibukawa, M., Raymond, C.
 and Haugen, E. D.

TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 149634)
 Kaul, R. K., Olson, M. V., Raymond, C. and Haugen, E. D.

AUTHORS Kaul, R. K., Olson, M. V., Raymond, C. and Haugen, E. D.
 TITLE Direct Submission
 JOURNAL Submitted (26-FEB-2002) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA

REFERENCE 3 (bases 1 to 149634)
 Kaul, R. K., Olson, M. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z.,
 Saenphimmachak, C., Phelps, K. A., Buckley, D., Kibukawa, M., Raymond, C.
 and Haugen, E. D.

TITLE Direct Submission
 JOURNAL Submitted (31-JUL-2002) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA

COMMENT On Jul 31, 2002 this sequence version replaced gi:18921343.
 ----- Genome Center
 Center: University of Washington
 Center Code: UWGC

Web site: <http://www.genome.washington.edu>

Contact: uwchgts@u.washington.edu

----- Project Information

Center project name: chr-3

Center clone name: RP11-739J4 (bc0790)

----- Summary Statistics

Sequencing vector: plasmid; 100% of reads

Chemistry: Dye-terminator ET; 5% of reads

Chemistry: Dye-terminator Big Dye; 43% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 149509 bases at least Q40

Consensus quality: 149632 bases at least Q30

Consensus quality: 149634 bases at least Q20

Insert size: 149634; sum-of-contigs

Quality coverage: 8.9x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': RP11-126H24 (UWGC:bc0241) AC027471

3': RP11-884K10 (UWGC:bc0575) AC012467

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part

of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.

EcoRI				HindIII				BglII			
SeqDerMap	FngrPrint	SeqDerMap	FngrPrint	SeqDerMap	FngrPrint	SeqDerMap	FngrPrint	SeqDerMap	FngrPrint	SeqDerMap	FngrPrint
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6	<800	6382	6521	2067	2120						
1476	1536	512	<800	6280	6434						
4410	4453	449	<800	160	<800						
589	<800	3754	3833	12532	12654						
1519	1536	2481	2481	12015	11825						
688	<800	2767	2826	8227	8201						
2527	2577	6254	6142	2137	2120						
6444	6507	481	<800	2999	3075						

86	<800	4792	4730	6988	7022
6129	6114	2471	2481	3538	3562
299	<800	822	834	10901	10734
1803	1796	2167	2146	2511	2407
172	<800	6141	6142	4290	4194
3531	3550	4509	4474	2314	2407
2454	2450	9111	9164	9252	9096
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2577	2577	303	<800	700	<800
18754	19107	14724	14557	1071	1033
2439	2450	4110	4079	1549	1496
106	<800	547	<800	11640	11825
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297	<800	5142	5034	4145	4194
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7635	7608	6135	6142	12012	11825
4807	4682	400	<800	3016	3075
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6538	6507	3378	3366		
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35	<800	4701	4730		
808	812	402	<800		
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AC012467	Homo sapiens	chr3 BAC RP11-884K10 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	177072 bp	DNA	linear	PRI 15-MAR-2002
AC012467	Homo sapiens	HTG.				
AC012467	Homo sapiens	ORGANISM				
AC012467	Homo sapiens	REFERENCE				
AC012467	Homo sapiens	AUTHORS				
AC012467	Homo sapiens	1 (bases 1 to 177072)				
AC012467	Homo sapiens	Muzny,D.M., Adams,C., Bailey,M., Barbara,J., Blankenburg,K., Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C., Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C., David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N., Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D., Forcun-Tansey,J., Frantz,P., Ganesh,R., Garcia,D.K., Gorrell,J.H., Gorrell,L.L., Guevara,W., Harris,K., He,X., Hernandez,J., Hodgson,A., Hognes,M., Holloway,C., Hosak,H., Jackson,L.B., Jackson,L., Jia,Y., Jones,M., Kelly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z., Lichtarge,O., Liu,J., Liu,W., Logan,O., Lozado,R.J., Lu,J., Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mei,G., Moore,S., Moorish,T., Morgan,M., Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S., Oswal,G., Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L., Quiles,M., Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S., Shah,E., Shen,H., Simon,M., Sparks,A., Stamps,A., Sucgang,R., Tabor,P., Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wabhan,M., Watlington,S., Weinstein,G., Weinstein,I.R., Williamson,A., Worley,K., Wren,J., Wrenford,G., Yu,W., Zhou,X., Naylor,S.L., Nelson,D. and Gibbs,R.				
AC012467	Homo sapiens	Unpublished				
AC012467	Homo sapiens	2 (bases 1 to 177072)				
AC012467	Homo sapiens	Worley,K.C.				
AC012467	Homo sapiens	Direct Submission				
AC012467	Homo sapiens	Submitted (28-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA				


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RESULT 4
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DEFINITION complete cds.
ACCESSION AF208110
VERSION AF208110.1 GI:9246432
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1828)
AUTHORS Tian.E., Sawyer.J.R., Largaespada,D.A., Jenkins,N.A., Copeland,N.G.
and Shaughnessy,J.D., Jr.
TITLE EVI27 encodes a novel membrane protein with homology to the IL17
receptor
JOURNAL Oncogene 19 (17), 2098-2109 (2000)
MEDLINE 20273223
PUBMED 10815801
REFERENCE
2 (bases 1 to 1828)
AUTHORS Shaughnessy,J.D. Jr.
TITLE Direct Submission
JOURNAL Submitted (24-NOV-1999) Myeloma and Transplantation Research
Center, University of Arkansas for Medical Sciences, 4301 W.
Markham St., Little Rock, AR 72212, USA
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DEFINITION Sequence 56 from Patent WO0100806.
ACCESSION AX061651
VERSION AX061651.1 GI:12406761
KEYWORDS SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1701)
AUTHORS dumas mine Edwards, J.B., Bougueleret, L. and Jobert, S.
TITLE Complementary dna's encoding proteins with signal peptides
JOURNAL Patent: WO 0100806-A 56 04-JAN-2001;
GENSET (FR)
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RESULT 6
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LOCUS Sequence 1 from Patent WO0190358.
DEFINITION AX350967
ACCESSION AX350967
VERSION AX350967.1 GI:18616343
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 unclassified.
AUTHORS Gorman, D.M.
TITLE Mammalian receptor proteins; related reagents and methods
JOURNAL Patent: WO 0190358-A 1-29-NOV-2001;
SCHERING CORPORATION (US)
FEATURES
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BASE COUNT 514 a 439 c 399 g 444 t
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Query Match 36.5%; Score 1041.8; DB 6; Length 1796;
Best Local Similarity 99.8%; Pred. No. 3.3e-259;
Matches 1043; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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LOCUS AX253204 1841 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 1 from Patent WO0168705.
ACCESSION AX253204
VERSION AX253204.1 GI:15986346
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1841)
AUTHORS Jing,S., Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S. and
Nguyen,H.Q.
TITLE IL-17 receptor like molecules and uses thereof
JOURNAL Patent: WO 0168705-A 1 20-SEP-2001;
Amgen Inc. (US)
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ORIGIN
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Best Local Similarity 99.7%; Pred. No. 8.7e-259;
Matches 1042; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 10	AX253207	2015 bp	DNA	linear	PAT 05-OCT-2001
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DEFINITION	AX253207				
ACCESSION	AX253207.1	GI:15986348			
VERSION					
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SOURCE	Homo sapiens				
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REFERENCE	1 (bases 1 to 2015)				
AUTHORS	Jing,S.; Medlock,B.; Yeh,R.; Silbiger,S.M.; Elliot,G.S. and Nguyen,H.Q.				
TITLE	Il-17 receptor like molecules and uses thereof				
JOURNAL	Patent: WO 0168705-A 4 20-SEP-2001;				
Amgen Inc. (US)					
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Best Local Similarity 99.7%; Pred. No. 8.8e-259;
Matches 1042; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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[illegible]

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QY	2319	CTTTTCTGCGATGATCTAAGAACCCAGATTATCTGCAAAATACGTGGTGGTCTACTTTT	2378
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Db 805	GTGCTCTGCCCAAAAAGGCGTCCCTTTCCTCTGGATAACAACAAAGCAAGCCCGGA	864			
Qy 1899	GGCTGGTGCTCTCCCTCTGCTCTGCTGGTGCCACATGGGTGCTGGTGCGAGGG	1958			
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GenCore version 5.1.4 p5_4578
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Searched: 16154066 seqs, 8097743376 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	423.4	21.6	425	9	AI158709
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ALIGNMENTS

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DEFINITION 602887278F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:504246
5', mRNA sequence.
ACCESSION BI103740
VERSION BI103740.1 GI:14554633
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 773)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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Location/Qualifiers

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Best Local Similarity 98.6%; Pred. No. 4.8e-133;
Matches 750; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
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RESULT 2
BB653710
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LOCUS BB653710 710 bp mRNA linear EST 26-OCT-2001
DEFINITION BB653710 RIKEN full-length enriched, adult male liver tumor Mus
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ACCESSION BB653710
VERSION BB653710.1 GI:16487538
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 710)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
        Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,
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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saiko,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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FEATURES

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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGCGCGCGCAACTCGAGTTTTTTTTTTTTTTTTTNN 3'], cDNA was
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5].
GAGAGAGATTCTCGAGTTAATAATTAATCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellular Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully acknowledge."

BASE COUNT 193 a 178 c 184 g 154 t 1 Others
ORIGIN

Query Match 34.0%; Score 668.4; DB 10; Length 710;
Best Local Similarity 99.1%; Pred. No. 3.1e-124;
Matches 694; Conservative 0; Mismatches 1; Indels 5; Gaps 2;

QY 1 GTGGCCAGTGGCGGCGCATGTTGCTAGTGTGCTGATCTTGCTGCATCGTGCAGGAGC 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2 GTGGCCAGTGGCGGCGCATGTTGCTAGTGTGCTGATCTTGCTGCATCGTGCAGGAGC 61
QY 61 GCCTGCTCGAGAGCGGACTTTCAGTGTGCTGCTGAGACAGGGCCATCTCCAGAGTGG 120
DB 62 GCCTGCTCGAGAGCGGACTTTCAGTGTGCTGCTGAGACAGGGCCATCTCCAGAGTGG 121
QY 121 ATGGTCCACACACACTCTCTCAGGAGACTTGGAGGAGCTTCAAGTGAATCTCGTCAAG 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
122 ATGGTCCACACACACTCTCTCAGGAGACTTGGAGGAGCTTCAAGTGAATCTCGTCAAG 181
QY 181 ACAAGTGTGGCAGCAGAGGAGTTTCAATTTTGATGAAATAGTGTGATATCTCGGGCA 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
182 ACAAGTGTGGCAGCAGAGGAGTTTCAATTTTGATGAAATAGTGTGATATCTCGGGCA 241
QY 241 GAGCCAGCATCGCTGTGAGGCGCCACAGATCTGCTGAGTGGCGGCAAAACACATG 300
DB 242 GAGCCAGCATCGCTGTGAGGCGCCACAGATCTGCTGAGTGGCGGCAAAACACATG 301
QY 301 AATTATACAGCTGTGAGGTGCACTACACAGAGGCTTCCAAAGCCAGACCAAGCT 360
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
302 AATTATACAGCTGTGAGGTGCACTACACAGAGGCTTCCAAAGCCAGACCAAGCT 361
QY 361 TCGGCGGCA----AATGACATTTCTCTATGTAGTGTCTTCCCTGTGGAGCTGAGCACTCT 416
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
362 TCGGCGGCAAAAGCAATGACATTTCTCTATGTAGTGTCTTCCCTGTGGAGCTGAGCACTCT 421
QY 417 CTATCTCATCAGCGCCCAATCAATCCCAATGCTATATGATGAGGACAGCCCTCTTT 476
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
422 CTATCTCATCAGCGCCCAATCAATCCCAATGCTATATGATGAGGACAGCCCTCTTT 481
QY 477 GTCTGTGAACCTTCACTCGCCAGGCTGCCTAAACACGTAATGAATATAAAAGCAGTG 536
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
482 GTCTGTGAACCTTCACTCGCCAGGCTGCCTAAACACGTAATGAATATAAAAGCAGTG 541
QY 537 CATGAGCGGGAAGCCTGTGGGACCCAGACATCACTGCTTGTGTAAGAACGAGAAGAT 596
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
542 CATGAGCGGGAAGCCTGTGGGACCCAGACATCACTGCTTGTGTAAGAACGAGAAGAT 601
QY 597 GGTGAAGTGAATTTCAACCAATCCCTTGGAAACAGATACAGATTTCTATCAACG 656
DB 602 GGTGAAGTGAATTTCAACCAATCCCTTGGAAACAGATACAGATTTCTATCAACG 661
QY 657 GGACACGACA-TTGGGGTGTCTAGAGTGTCTGGAGATTA 695
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
662 GGACACGACATTTGGGGGTTCTAGAGTGTCTGGAGATTA 701

RESULT 3
LOCUS BB667509 728 bp mRNA linear EST 24-OCT-2001
DEFINITION BB667509 RIKEN full-length enriched, adult male liver tumor Mus
musculus cDNA clone C730019M05 3', mRNA sequence.
ACCESSION BB667509

VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES
source

BB667509.1 GI:16398958
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Bases 1 to 728)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Iehi, Y., Ito, M., Kawai, J., Kawai, J., Kondo, H., Kouda
M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, I., Aizawa
K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
Location/Qualifiers
1..728
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="C730019M05"
/clone_lib="RIKEN full-length enriched, adult male liver
tumor"
/sex="male"
/tissue_type="liver tumor"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5].
GAGAGAGAGCGGCGCACTCGAGTTTTTTTTTTTTTTVN 3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5].

Best Local Similarity 99.6%; Pred. No. 2e-101; Matches 556; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGGCCAGTGGCGGCGCATGTTGCTAGTGTCTGCTATCTTGGCTGCATCGTCAGGAGC 60
 Db 89 GTGGCCAGTGGCGGCGCATGTTGCTAGTGTCTGCTATCTTGGCTGCATCGTCAGGAGC 148
 Qy 61 GCCTCTGCTCGAGAGCGGCACTATTAGTGTGGCTCTGAGACAGGGGCATCTCCAGAGTGG 120
 Db 149 GCCTCTGCTCGAGAGCGGCACTATTAGTGTGGCTCTGAGACAGGGGCATCTCCAGAGTGG 208
 Qy 121 ATGGTCCACACACACTCACTCAGAGAGCTTGGAGGACCTCCAAAGTGAATCTGTCAG 180
 Db 209 ATGGTCCACACACACTCACTCAGAGAGCTTGGAGGACCTCCAAAGTGAATCTGTCAG 268
 Qy 181 ACAAGTGTGGCAGCAGAGAGTTCCTCAATTTTGTATGAACATAGCTGGATCTCCGGGCA 240
 Db 269 ACAAGTGTGGCAGCAGAGAGTTCCTCAATTTTGTATGAACATAGCTGGATCTCCGGGCA 328
 Qy 241 GAGCCAGAGTCCGCTTGTGTAAGGCGCACCAAGATCTGGGTGAGTGGCAAAACCAACATG 300
 Db 329 GAGCCAGAGTCCGCTTGTGTAAGGCGCACCAAGATCTGGGTGAGTGGCAAAACCAACATG 388
 Qy 301 AATTCTACAGCTGTGTAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACCAAGACCT 360
 Db 389 AATTCTACAGCTGTGTAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACCAAGACCT 448
 Qy 361 TCGGCGGCAATGGAATCTCTATGTAGGCTTCCCTGTGGAGTGGAGCTGCTCTAT 420
 Db 449 TCGGCGGCAATGGAATCTCTATGTAGGCTTCCCTGTGGAGTGGAGCTGCTCTAT 508
 Qy 421 CTCATCAGCGGCCATTAACATCCCAATGCTAATATGAATGAGACAGCGCTTCTTTGCT 480
 Db 509 CTCATCAGCGGCCATTAACATCCCAATGCTAATATGAATGAGACAGCGCTTCTTTGCT 568
 Qy 481 GTGAATCTCACTCGCAGGCTGCTTAACACAGCTAATGAATATATAAAGCAGTGCAT 540
 Db 569 GTGAATCTCACTCGCAGGCTGCTTAACACAGCTAATGAATATATAAAGCAGTGCCT 628
 Qy 541 GAGCGGGAAGCTGTGG 558
 Db 629 GAGCGGGAAGCTGTGG 646

RESULT 6
 AL535617
 LOCUS AL535617 LTI FL013 FBrn1 Homo sapiens cDNA clone CS0DF016YG03 5
 DEFINITION prime, mRNA sequence.
 ACCESSION AL535617
 VERSION AL535617.1 GI:12799110
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 869)
 AUTHORS Li W.B., Gruber C., Jessee J. and Pollayes D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 source
 1..869
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DF016YG03"
 /clone.lib="LTI FL013 FBrn1"
 /dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
 /lab_host="DH10B"

/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 240 a 210 c 208 g 191 t 20 others
 ORIGIN
 Query Match 25.9%; Score 508.2; DB 9; Length 869;
 Best Local Similarity 76.0%; Pred. No. 4.2e-92;
 Matches 659; Conservative 17; Mismatches 175; Indels 16; Gaps 4;
 Qy 15 GGCCAGTGTGCTAGTGTGCTGATCTTGGCTGCATCGTCAGAGGCGCCCTGCTCGAGA 74
 Db 1 GGCGAKGTGCGTGTGCTGCTAAAGCTGGCCGCTGTGCAGAGGCGCGTACCCCGAGA 60
 Qy 75 GCCGACTATTGCTGCTGCTGTGAGACAGGGCCATCTCCAGAGTGGATGGTCCACACAC 134
 Db 61 GCCGACCGCTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGSKAACACATGA 120
 Qy 135 ACTCACTCCAGAGACTTGGAGGACCTCCAAGTGGAACTCGTCAAGACAAAGTGTGGCAGC 194
 Db 121 TCTAATCCGGGAGACTTGGAGGACCTCCGAGTAGAACCTGTTACAACTAGTGTGCAAC 180
 Qy 195 AGAGAGTGTTCATTTTGTATGAACATAAGCTGGATATCTCCGGGAGAGCGCCAGATCGG 254
 Db 181 AGGGGACTATTCAATTTTGTATGAATGTAAGCTGGGTATCTCCGGGAGATGCCAGATCGG 240
 Qy 255 CTGTTGAAGGCCCAACAGATCTCGTGAGTGGCAAAACCAACATGATTCATACAGCTG 314
 Db 241 CTGTTGAAGGCCCAACAGATTTGTGTGANGGGCAAAAGCAACWTCCAGTCTCTACAGCG 300
 Qy 315 TGTGAGGT-GCAACTACACAGAGGCC-----TTCAAAGCCAGACCAAGCTTCCGGCGG 368
 Db 301 TGTGAGGTAGCAATTACACAGAGACATATCCAGACTCTAGACCAGACCTCTGGGG 360
 Qy 369 CAATGGACATTTCTCTATGAGTTCCTCTGTGAGTGGAGTGCATCTCTAT-CTCATCA 427
 Db 361 TAAATGGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCAATTG 420
 Qy 428 GCGCCATAACATCCCCAATCTAATGATGAGGAGCGCCCTCTTTGCTGTGAACT 487
 Db 421 GGGCCCAWAATAMWCCCTAATGCAATATGAATGAAGATGGCCCTTCCATGTGTGAAAT 480
 Qy 488 TCACCTCGCCAGGCTGCCCTAAACCAACGTAATGAATAATAAAGCAGTGCATCTGAGCGG 547
 Db 481 TCACCTCACAGGCTGCCCTAGACACATATGAATAATAAAGTGTCTCAAGCGG 540
 Qy 548 GAAAGCTGTGGAGCCAGACATCACTGCTCTTAAAGAAAGCAGAGAGATGTTGAAGTGA 607
 Db 541 GAAAGCTGTGGAGCCGAAACATCACTGCTTGAAGAAAGATGARGAGACAGTGAAGTGA 600
 Qy 608 ATTTACACAACTCCCTTGGAAACAGATACAGATTTCTTCTTCAAGCGGACAGCAT 667
 Db 601 ACTTCACAACTCCCTTGGAAACAGATATATGCTCTTATCCAAACARMACATCA 660
 Qy 668 TGGGCTTTCTAGAGTGTCTG-----AGAATAAACTGATGAGGAGCTGTGTAGCCA 718
 Db 661 TCGGGTTTCTCAGGTGTTTGGCCACACAGAGAGAAACAAACCGAGCTTCAGTGGTGA 720
 Qy 719 TCCCGGTGACTGAGAGAGTGAAGTGGGTGTTGAGTGCACCCCATATTTTACATACCT 778
 Db 721 TCCAGTGAAGTGAAGTGTGCTACGGTGCAGTGCATCTTCTTCTTCTTCTTCTTCTTCT 780
 Qy 779 GCGCAATGCTGATCGAGCGGAGGAGCAGTGTGCTTTGCTCAGAGACAGTGTCTC 838
 Db 781 GTGGCAGCGWCTGATCCGATATAAGGAAACAGTGTGCTCTGCCCAACAAACAGCGCTCC 840

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

MGI:1453973
 Seq primer: -40UP from Gibco
 High quality sequence stop: 367.

FEATURES

Location/Qualifiers
 1. .431
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:3811861"
 /clone_lib="NCI_CGAP_Li10"
 /sex="female"
 /dev_stage="10 weeks"
 /lab_host="DH10B (11 phage-resistant)"
 /note="Organ: liver; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.6 kb. Library constructed by Life
 Technologies."

BASE COUNT 104 a 108 c 119 g 100 t

Query Match 22.0%; Score 431; DB 12; Length 431;
 Best Local Similarity 100.0%; Pred. No. 1.6e-76;
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 TTCCAGTACGTCGCGACCTTTGTGACAGTCCCTGTGGCCACAATGAGGCGGCCA 1255
 DB 431 TTCCAGTACGTCGCGACCTTTGTGACAGTCCCTGTGGCCACAATGAGGCGGCCA 372
 QY 1256 GGAGAACTCTCAGGATCTGTCCTCTTGCCTTAACTCTTTGTAGTATTTCAGCA 1315
 DB 371 GGAGAACTCTCAGGATCTGTCCTCTTGCCTTAACTCTTTGTAGTATTTCAGCA 312
 QY 1316 GCAGAGCGATCTGCACAAATACCTGGTGTCTATCTTGGGGGAGCAGACCTCAAGGGC 1375
 DB 311 GCAGAGCGATCTGCACAAATACCTGGTGTCTATCTTGGGGGAGCAGACCTCAAGGGC 252
 QY 1376 ACTAATGCTGAGTGTCTGCGCCCAATATCATCTCATGAAGGAGCGCAGCTTTCC 1435
 DB 251 ACTAATGCTGAGTGTCTGCGCCCAATATCATCTCATGAAGGAGCGCAGCTTTCC 192
 QY 1436 ACACAACTTCTCAAGGCTACGACAGATGTCAGTGAAGAAAGCTCACAAGCTGCC 1495
 DB 191 ACACAACTTCTCAAGGCTACGACAGATGTCAGTGAAGAAAGCTCACAAGCTGCC 132
 QY 1496 ATGATAGCTGTTTACCCCTTTGTATGCACCCGGGGGAATAGAGACTCTGAAGCTTCTTAC 1555
 DB 131 ATGATAGCTGTTTACCCCTTTGTATGCACCCGGGGGAATAGAGACTCTGAAGCTTCTTAC 72
 QY 1556 TCTCCCTTCAGTGACAAATGCTGTGTGAGACTCTGAATGTGGGAGAGGCTGTGTG 1615
 DB 71 TCTCCCTTCAGTGACAAATGCTGTGTGAGACTCTGAATGTGGGAGAGGCTGTGTG 12
 QY 1616 GAGGTAGTCT 1626
 DB 11 GAGGTAGTCT 1

RESULT 9
 LOCUS A1158709 425 bp mRNA linear EST 30-SEP-1998
 DEFINITION u01d07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
 IMAGE:1345453 5', mRNA sequence.
 ACCESSION A1158709
 VERSION A1158709.1 GI:3687178
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 425)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

TITLE

The WashU-HHMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu

JOURNAL

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:694245
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 402.

FEATURES

Location/Qualifiers
 1. .425
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:1345453"
 /clone_lib="Soares_thymus_2NbMT"
 /sex="male"
 /tissue_type="Thymus"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /note="Vector: p7T3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer 15'
 TGTACCAATCTGAAGTGGAGGCGCGCTTTTTTTTTTTTTTTTTTTTTT
 3'; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. RNA
 provided by Dr. Bertrand Jordan. Library went through two
 rounds of normalization, and was constructed by Bento
 Soares and M.Fatima Bonaldo."
 BASE COUNT 117 a 107 c 103 g 98 t

ORIGIN

Query Match 21.6%; Score 423.4; DB 9; Length 425;
 Best Local Similarity 99.8%; Pred. No. 5.3e-75;
 Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1306 GATTTCAGCAGCCAGACGATCTGCACAAATACCTGGTGTCTATCTTGGGGGAGCAGAC 1365
 DB 1 GATTTCAGCAGCCAGACGATCTGCACAAATACCTGGAGGTCTATCTTGGGGGAGCAGAC 60
 QY 1366 CTCAAAGCGCATTAATGCGCTGAGTGTCTGCCCCCAATATCATCTCATGAAGAGCGCC 1425
 DB 61 CTCAAAGCGCATTAATGCGCTGAGTGTCTGCCCCCAATATCATCTCATGAAGAGCGCC 120
 QY 1426 ACAGCTTCCACACAGAACTTCTCAAGGCTACGAGAGCATGTCAGTGAAGAAAGCTCA 1485
 DB 121 ACAGCTTCCACACAGAACTTCTCAAGGCTACGAGAGCATGTCAGTGAAGAAAGCTCA 180
 QY 1486 CAAGCTTCGCATGATAGTGTTCACCTTGTAGTCCACCCCGGGGAATAGAGACTCTCAA 1545
 DB 181 CAAGCTTCGCATGATAGTGTTCACCTTGTAGTCCACCCCGGGGAATAGAGACTCTCAA 240
 QY 1546 GCCTTCCTACTCTCCCTCCAGTGACAAATGCTGTGTGACGACTCTGAAATGTGTGGAG 1605
 DB 241 GCCTTCCTACTCTCCCTCCAGTGACAAATGCTGTGTGACGACTCTGAAATGTGTGGAG 300
 QY 1606 AGGCTGTGTGGAGTGTGTATGTACAAACTCTCTTTAAACTGGAGTTTGCAAGTCA 1665
 DB 301 AGGCTGTGTGGAGTGTGTATGTACAAACTCTCTTTAAACTGGAGTTTGCAAGTCA 360

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QY 1666 ACCTGACATACAGCGCTGAGGCTAGTTCATTCGCTGGATTATGAAGACACACAGTTAC 1725
Db. 361 ACCTGACATACAGCGCTGAGGCTAGTTCATTCGCTGGATTATGAAGACACACAGTTAC 420

QY 1726 AGACA 1730
Db. 421 AGACA 425

RESULT 10
LOCUS AW675096 561 bp mRNA linear EST 11-APR-2000
DEFINITION bb40e05.y1 NIH MGC 12 Homo sapiens cDNA clone IMAGE:2985728 5'
similar to TR:O43844 O43844 IL-17 RECEPTOR.; mRNA sequence.
ACCESSION AW675096
VERSION AW675096.1 GI:7540331
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 561)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other ESTs: bb40e05.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 441.
FEATURES
source
1..561
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2985728"
/clone_lib="NIH MGC 12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
BASE COUNT 146 a 143 c 141 g 130 t 1 others
ORIGIN
Query Match 20.3%; Score 398.4; DB 10; Length 561;
Best Local Similarity 81.8%; Pred. No. 5.2e-70;
Matches 459; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 13 CGGGCATGTGTCTAGTGTGTCTGATCTGGCTGCATCGTGAGGAGCGCCCTCGCTCGA 72
Db. 1 CGGGCATGTGTCTAGTGTGTCTGATCTGGCTGCATCGTGAGGAGCGCCCTCGCTCGA 60

QY 73 GAGCCGACTATTTCAGTGTGGCTCTGAGACAGGGGCCATCTCCAGAGTGGATGTTCCAAAC 132
Db. 61 GAGCCGACGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGTTCAACAT 120

QY 133 ACATCTACTCCAGGAGACTTGGAGGACCTCCAAAGTGGAACTGCTCAAGACAGTGTGGCA 192
Db. 121 GATCTAATCCCGGAGACTTGGAGGACCTCCCGAGTAGAACCTGTTACAACTAGTGTGCA 180

QY 193 GCAGAGGAGTTTCAATTTTGTATGAACATAAGCTGATCTCCGGGCGAGCGCCAGCATC 252
Db. 181 ACAGGGGACTATTCAATTTTGTATGAATGAAGCTGGGTACTCCGGGCGAGTCCAGCATC 240

QY 253 CGCTTTGTAAGGCCACCAAGATCTCGTGTAGTGGCAAAAAACAACATGAATTCATACAGC 312

```

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Db. 241 CCGCTTGTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCAGTCTTACAGC 300
QY 313 TGTGTGAGTGCAAACTTACACAGAGCGCTTCCAAAGCCAGACAGACCTTCCGGCGGCAAA 372
Db. 301 TGTGTGAGTGCAATTTACACAGAGCGCTTCCAGACTCAGACCAGACCCCTCTGTGTGTA 360
QY 373 TGGACATTTCTCTATGTAGGCTTCCCTGTGTGAGCTGAGCACTCTCTATCTATCAGCGCC 432
Db. 361 TGGACATTTCTCTATCATCGGCTTCCCTGTGTGAGCTGAGCACTCTATTTCTATTTGGGCG 420
QY 433 CATACATCCCCCAAGCTTAATGAATGAGGAGACGCCCTTCTTTCTGTGTAACCTTCCAC 492
Db. 421 CATATATTTCTTAATGCAAAATATGAATGAATGAGGAGCTTCCATGCTGTGTAATTCAC 480
QY 493 TCGCCAGGCTGCTTAAACCCACGTAATGAATAATAAAAGCAGTGCACCTGAGCGGGAAGC 552
Db. 481 TCACCAGGCTGCTAGACACACATATGAATAATAAAAGTGTGTCAAGCGCGGAAGC 540
QY 553 CTGTGGGACCCAGACATCACT 573
Db. 541 CTGTGGGATCCGAACATCACT 561

RESULT 11
LOCUS AV709899 703 bp mRNA linear EST 09-OCT-2000
DEFINITION AV709899 ADC Homo sapiens cDNA clone ADCACB04 5', mRNA sequence.
ACCESSION AV709899
VERSION AV709899.1 GI:10728055
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 703)
AUTHORS Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao,
H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z.,
Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu,
G., Hu, R., Chen, J., Chen, Z. and Han, Z.
TITLE Homo sapiens cDNA ADC clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
1..703
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADCACB04"
/clone_lib="ADC"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site 1: EcoRI; Site 2:
XhoI"
BASE COUNT 186 a 172 c 166 g 177 t 2 others
ORIGIN
Query Match 19.7%; Score 386; DB 10; Length 703;
Best Local Similarity 75.7%; Pred. No. 1.5e-67;
Matches 508; Conservative 0; Mismatches 151; Indels 12; Gaps 2;

QY 294 CAACTGATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCTTCCAAAGCCAGAC 353
Db. 2 CAACTTCAGTCTTACAGCTGTGTGAGGTGCAATACACAGAGGCTTCCAGACTCAGAC 61

QY 354 CAGACCTTCCGGCGGCAAAATGACATTTCTCTATGTAGGCTTTCCCTGTGTGAGCTGAGC 413

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Db	62	CAGACCCCTCTGGTGAATAGGACATTTTCTATATCGGCTTCCCTGTAGAGCTGAACAC	121
Qy	414	TCTCTATCTCATCAGCCCCATAACATCCCCAATGCTAATATGAATGAGGACAGCCCTTC	473
Db	122	AGTCTATTTTCAITGGGCCCCAATAATTTCTAATGCAATATGAATGAAGATGGCCCTTC	181
Qy	474	TTTGTGCTGGAACCTTCACTCGCCAGGCTGCCTAAACCAAGTAAATGAAATATATAAAGCA	533
Db	182	CATGCTCTGGAATTTTCACTTCACGAGCTGCCTAGACCATATTAATGAAATATATAAAAAA	241
Qy	534	GTGCACCTGAGCGGGGAAGCCCTGTGGGACCCAGACATCACTGCTTGTAAAAAGAACGAGAA	593
Db	242	GTGTGTCAAGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAAGAAATGAGGA	301
Qy	594	GATGGTTGAAGTGAATTTTCAACACCAATCCCTTGGAAACAGATACAGATCTCATTTCA	653
Db	302	GACAGTAGAAGTGAACCTTCAACACCACTCCCTCGGGAAACAGATACATGGCTCTTATCCA	361
Qy	654	ACGGGACACGACATTTGGGGTTTTCTAGAGTGTGG-----AGCAATAAATCATGTAG	704
Db	362	ACACAGCACTATCATCGGTTTTTCTCAGGTGTTTGAGCCACACCAAGAGAAACAAACGG	421
Qy	705	GAGCTCTGTAGCCATCCCGTGATCAGGAGAGTGAAGGTGCGGTGGTTTCACTGACCCC	764
Db	422	AGCTTCAGTGGTGATTCAGTGCATGGGGATGTGAAGGTGCTACGCTGCAGCTGACTCC	481
Qy	765	ATATTACATACCTCGGGCAATCACTGCAATCCGACGAGGAGGACAGTTGTCTTTGTCTC	824
Db	482	ATATTTTCTACTTGTGGCAGCACTGCATCCGACATAAAGGNACAGTTGTGCTCTGCCCC	541
Qy	825	AGAGACAAGTGCTCCCATCCCTCCAGATGACACAGACGCATGCTGGGAGGCTGGCTGCC	884
Db	542	ACAAACAGGGGTNCCCTTTCTCTGGATACAAACAAAGCAAGCCGGGAGGCTTGGCTGC	601
Qy	885	TCTCTTCCCTGGT---CTGCTGGTGCTGTGGGTGCTGGCAGCTGGGATCTACCTAAC	941
Db	602	TCCTCTCTGCTGCCTTTGCTGTGGCCACATTTGGTGTGGTGGCAGGATCTATCTAAT	661
Qy	942	TTGGAGGCAAG	952
Db	662	GTGGATGCAG	672

RESULT 12
BG384365
LOCUS
BG384365 551 bp mRNA linear EST 12-MAR-2001
DEFINITION 303436 MRC 1P1G Sus scrofa cDNA 5', mRNA sequence.

BACKWARD: GTTTCCCGAGTCACGACG	
Plate: 91	row: J column: 1
Seq primer: ATTTAGTGACACTATAG.	
FEATURES	Location/Qualifiers
source	1..551
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	/db_xref="taxon:9823"
	/clone_lib="MARC iPig"
	/tissue_type="pooled"
	/lab_host="DH10B"
	/notes="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
	Library made from pooled tissue from day 11, 13, 15, 20,
	and 30 embryons."
BASE COUNT	140 a 138 c 150 g 123 t
ORIGIN	
Query Match 19.4%; Score 381.4; DB 12; Length 551;	
Best Local Similarity 81.4%; Pred. No. 1.3e-66;	
Matches 442; Conservative 0; Mismatches 101; Indels 0; Gaps	
Qy	1 GTGCGCAGTGCCGGGCATGTTGTCTAGTCTTCTCTCATCTTGGCTGCATCGTGCAGGAGC 60
Db	9 GCGGGAAGTGCCTCCCGCGATGTTACTAGTGTCTCTGAGCTGCGCCGGCTGTGCTGGGT 68
Qy	61 GCCCTGGCTCGAGAGCCGACTATTCTAGTGTGGCTCTGAGACAGGGCCATCTCCAGAGTGG 120
Db	69 GCCATGCTCCAGAGCCGCAATTCCTAGTGTGGCTCTGAGCTTGAGCTGCTCTCCAGAATGG 128
Qy	121 ATGTTCAACACACACTCACTCCAGAGACTTTGAGGACCTCCAAGTGAACCTGTCGTAAG 180
Db	129 ATGTTTCGACACGCTCTGACCCAGGAGACTTGAGGGACCTCCGAGTGGAACTATTAAA 188
Qy	181 ACAAGTGTGGCAGCAGAGGAGTTTTCAATTTTCATGAACATAAGCTGGATACTCCGGGCA 240
Db	189 AGCAGTGTTCGAGTGGAGGACTATTCAATTTTGAATGAACATAAGCTGGATACTCCGGGCA 248
Qy	241 GAGCCAGCATCCGCTTTGTTGAAGGCCACCAAGATCTGCTGAGTGGCGCAAAACCAATG 300
Db	249 GATGCCAGTATCCGATTTGTTGAAGGCCACCAAGATCTGTGTGACGGCAAGAGCCAGAA 308
Qy	301 AATTCTACAGCTGTGTGAGGTGCACTACACAGAGCCCTTCCNAAGCCAGACCACT 360
Db	309 CAGACCTTACAGCTGCGTGGAGTGCATTTACCTGAGGCCCTTCCAGACTCAGACCACT 368
Qy	361 TCCGGCGGCAAAATGGACATTTCTCTATGTAGGCTTCCCTGTGAGCTGAGCACTCTCTAT 420
Db	369 TCTGGCGGCAAAATGGATGTTTCTCTAGTAGGCTTTCCAGTAGAGCTGAATACACGCTAT 428
Qy	421 CTCATCAGGCCCCATAACACTCCCAATGCTAATGAATGAGGACAGGCCCTTTCTTTGCT 480
Db	429 TTCAATTGAGCCCATTAATATCCCAATGCAAAATATGAACGAAGATGGCCCTCTTTGGCT 488
Qy	481 GTGAACCTTCACTTCGCCAGGCTGCCTTAACACCGTAAATGAATATATAAAGCAGTGCACT 540
Db	489 GTGAACCTTCACTTCCAGGCTGCCTGGACCGCATTAATGAATATACAAAAAAGTGCACT 548
Qy	541 GAG 543
Db	549 GAG 551
RESULT 13	
BI360842	588 bp mRNA linear EST 01-AUG-20
LOCUS	BI360842
DEFINITION	388904 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION	BI360842
VERSION	BI360842.1 GI:15056870
KEYWORDS	EST.
SOURCE	Pig.
ORGANISM	Sus scrofa
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
	1 (bases 1 to 588)

AUTHORS Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.

TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine

JOURNAL Unpublished (2000)

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers
FORWARD: AGCAACAGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 141 row: I column: 23
Seq primer: ATTAGTGACACTATAG.

FEATURES
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/db_xref="taxon:9823"
/clone_lib="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 146 a 151 c 165 g 126 t

ORIGIN

Query Match 19.3%; Score 378.8; DB 13; Length 588;
Best Local Similarity 81.2%; Pred. No. 4.4e-66;
Matches 440; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 1 GTGGCAGTGGCGGGCCATGTTGCTAGTGTCTGCTGATCTTGCTGCTGATCGTCAGAGC 60
DB 47 GCGGGAAGTCGCCCGCGATGTTACTAGTGTCTGCTGAGCTGCGCGCTGCTGGGT 106

QY 61 GCCTCTCGTGGAGCGGACTTTCAGTGTGGCTCTGAGCAGGGCCACTCCAGAGTGG 120
DB 107 GCATCGCTCCAGAGCGCAATTCAGTGTGGCTCTGAGCCTGGACTGTCAGAAATGG 166

QY 121 ATGGTCCAAACACACACTCACTCAGAGACTTGAGGCACTCCAACTGGAACCTCGTCAAG 180
DB 167 ATGGGTGACACCGCTCTGACCCAGAGACTTGAGGCACTCCGAGTGAACCTATTAA 226

QY 181 ACAAGTGTGGCAGCAGAGAGTTTCAATTTGATGAAATAGCTGGATCTCCGGCA 240
DB 227 AGCAGTGTTCAGTGGAGGACTATTCAATTTGATGAAATAGCTGGATCTCCGGCA 286

QY 241 GAGCCAGCATCGCTTGTGTGAGGCCACCAAGATCTGGTGTGGCGCAAAACACATG 300
DB 287 GATGCCAGTATCGGATGTTGAGGCCACCAAGATCTGTGTGAGCGGCAAGAGCCAGAG 346

QY 301 AATTATACAGCTGTGTGAGTGCAACTACACAGAGCGCTTCCAAAGCCAGACCACT 360
DB 347 CAGACCTACAGCTGCTGAGGTGCATTACACTGAGGCTTCCAGACTCAGACCACT 406

QY 361 TCGGGCGGAATGGAATCTCTCTATGAGGCTTCCCTGTGAGCTGAGCACTCTCTAT 420
DB 407 TCTGGCGGCAATGGAATGTTTCTACGTAGGCTTCCAGTAGCTGAATACAGCTAT 466

QY 421 CTCATCAGCGCCATACATCCCAATGCTATATGAAATGAGACAGCCCTCTTGTCT 480
DB 467 TTCAITGGAGCCCATTAATATCCCAATGCAATATGAAATGAGATGCGCCCTCTTGGCT 526

QY 481 GTGAACCTCCACCTCGCAGGCTGCTTAAACACAGTAAATGAAATATATAAAGCAGTCACT 540
DB 527 GTGAACCTCCACCTCGCAGGCTGCTTAAACACAGTAAATGAAATATATAAAGTCACT 586

QY 541 GA 542
DB 587 GA 588

RESULT 14
AA562342
LOCUS
DEFINITION
V122H03.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
IMAGE:973013 5', mRNA sequence.

ACCESSION AA562342
VERSION AA562342.1 GI:2333807
KEYWORDS EST.
SOURCE House mouse.
ORGANISM Mus musculus

REFERENCE
1 (bases 1 to 370)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisels, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

AUTHORS
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

TITLE
JOURNAL
COMMENT
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:553741
Putative full length read
vector to vector length is 377
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 326.

FEATURES
Location/Qualifiers
1..370
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/clone_lib="Stratagene mouse Tcell 937311"
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/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'."

BASE COUNT 105 a 73 c 91 g 101 t

ORIGIN

Query Match 18.7%; Score 366.8; DB 9; Length 370;
Best Local Similarity 99.5%; Pred. No. 1.3e-63;
Matches 368; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1586 GACTCTGAAATGTGGGAGAGGCTGTGTGGAGGTAGTGTATGTACAACTTGCTTTAA 1645
DB 1 GACTCTGAAATGTGGGAGAGGCTGTGTGGAGGTAGTGTATGTACAACTTGCTTTAA 60

QY 1646 AACTGGAGTTTCAAGTCAACCTGAGCATACACCCCTGAGGCTAGTCACTGGCTGGATT 1705
DB 61 AACTGGAGTTTCAAGTCAACCTGAGCATACACCCCTGAGGCTAGTCACTGGCTGGATT 120

QY 1706 TATGAAGCAACACAGTGTACAGACAATATGAGTGGGACCTACATTTGGGATATACCCAA 1765
DB 121 TATGAAGCAACACAGTGTACAGACAATATGAGTGGGACCTACATTTGGGATATACCCAA 180

QY 1766 AGCTGGGTAAATGATTATCACTGAGAACCAACGCACTCTGGCCATGAAGTAATACGGCACTT 1825

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Db 181 AGCTGGTAAATGATATCACTGAGAACCCAGCCTCTGGCCATCAGGTAATACGGCACTT 240
QY 1826 CCCTGTCAGGCTGCTGTGAGGTTGGTCTCTTGCACATGCCATGCTCTATGCTGCAC 1885
Db 241 CCCTGTCAGGCTGCTGTGAGGTTGGTCTCTTGCACATGCCATGCTCTATGCTGCAC 300
QY 1886 GTAGACCGTTTGTAACTTTTAACTTGTAAATGTAATATCCGTTTGGGAAGCTCTCAAA 1945
Db 301 GTAGACCGTTTGTAACTTTTAACTTGTAAATGTAATATCCGTTTGGGAAGCTCTCAAA 360
QY 1946 AAAAAA 1955
Db 361 AAAAAA 370

RESULT 15
BM693867
LOCUS
DEFINITION
  UI-E-DWI-ah-e-1-22-0-UI.t1 UI-E-DWI Homo sapiens cDNA clone
  UI-E-DWI-ah-e-1-22-0-UI 5', mRNA sequence.
ACCESSION
  BM693867
VERSION
  BM693867.1 GI:19007125
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 652)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  97044477
  Contact: Soares, MB
  Program for Rat Gene Discovery and Mapping
  University of Iowa
  451 Eckstein Medical Research Building Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: msoares@blue.weeg.uiowa.edu
  Tissue Procurement: Dr. Gregg Hageman
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Researchers may obtain clones from Research
  Genetics (www.resgen.com).
  Seq primer: M13 Reverse.
  Location/Qualifiers
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      /organism="Homo sapiens"
      /db_xref="taxon:9606"
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      /clone_lib="UI-E-DWI"
      /tissue_type="lens"
      /dev_stage="adult"
      /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
      /note="organ: eye; Vector: pT73-Pac (Pharmacia) with a
      modified polylinker; Site_1: EcoR I; Site_2: Not I;
      UI-E-DWI is a normalized cDNA library containing the
      following tissue(s): lens. The library was constructed
      according to Bonaldo, Lennon and Soares, Genome Research,
      6:791-806, 1996. First strand cDNA synthesis was primed
      with an oligo-dT primer containing a Not I site. Double
      stranded cDNA was ligated to an EcoR I adaptor, digested
      with Not I, and cloned directionally into pT73-Pac
      vector. The oligonucleotide used to prime the synthesis of
      first-strand cDNA contains a library tag sequence that is
      located between the Not I site and the (dT)18 tail. The
      sequence tag for this library is CGATTAGCGA. This library
      was created for the program, Gene Discovery in the Visual
      System, supported by National Eye Institute (NEI)."
    188 a 167 c 135 g 162 t
  
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BASE COUNT

ORIGIN

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Query Match      18.6%; Score 366; DB 14; Length 652;
Best Local Similarity 76.0%; Pred. No. 1.6e-63;
Matches 465; Conservative 0; Mismatches 145; Indels 2; Gaps 1;

QY 965 AGACGTCTCTTTCTTATTTCCACCATGCTCTGCCCTCATTAAGGTCCTGTGGTTTATC 1024
Db 1 AGAAGACTCTCTTTTCTTACCAACACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACC 60
QY 1025 CTTCTGAGATATGTTTTCATATCACACGCTGTGCGTCTACTGACTTCTTCAAAACTACT 1084
Db 61 CATCTGAATATGTTTCCATCATCACAAATTTGTTACTTCACTCAATTTCTTCAAAACCA 120
QY 1085 GCAGAAGTCAGGTCATCTTGAATAATGCAGAAAAGAAATCCCGAGATGGGGCCG 1144
Db 121 GCAGAAGTCAGGTCATCTTGAATAATGCAGAAAAGAAATAGCAGAGATGGGGTCCAG 180
QY 1145 TACAGTGGCTGACCACTCAGAAAGCAAGCGGCGAGATAAAGTGGTCTTCTTCTTCCAGTG 1204
Db 181 TGCAGTGGCTTGCCTCACTCAAAAGAGGCGAGACAAAGTCTCTTCTTCTTCTTCCAA 240
QY 1205 AGTCCCGACCTTTGTGACAGTGCCTGTGCGCAACAATGAGGGCGAGCCAGGAGAACT 1264
Db 241 ACGTCAACAGTGTGTGCGATGTGTCTGTGGCAAGAGCGAGGGCGATCCCACTGAGA 300
QY 1265 CTCAGATCTGTCTCTCTTCTTAACTCTTTTGTAGTATTTTACAGCAGCAGACGC 1324
Db 301 CTCAAGACCTTCTCTCTTCTTAACTCTTTTCTGAGTATCTTGAAGCCAGATTC 360
QY 1325 ATCTGCACAAATFACCTGGTGGTCTATCTTGGGGGAGCAGACCTCAAGGCGACTATAATG 1384
Db 361 ATCTGCACAAATFACCTGGTGGTCTATCTTGAAGATTTGATACAAAGACGATTACA 420
QY 1385 CCTGAGTGTCTGCCCCCAATATCATCTCATGAAGAGCGCCACAGCTTTCCACAGAAC 1444
Db 421 CTCTCAGTGTCTGCCCCCAAGTACCACCTCATGAAGATGCCACTGCTTTCTGTGAGA 480
QY 1445 TTCTCAAGCTACGAGAGCATGTGAGTGAAGAAAGCTTCAAGCCCTGCCATGATAGCT 1504
Db 481 TTCTCCATGTCAAGCAGCAGGTTGTGAGGAGAAAGATCAAGCCCTGCCACGATGGCT 540
QY 1505 GTTCAACCTTGTAGTCCACCCCGGGGAA--TAGAGACTCTTGAAGCTTCTTCTCTCCCT 1562
Db 541 GCTGCTCTTGTAGCCCAACCCATGAGAGCAAGACCTTAAAGGCTTCTTATCCACCA 600
QY 1563 TCCAGTGAACA 1574
Db 601 ATTACAGGGAAA 612
  
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Search completed: May 28, 2003, 10:13:27
Job time : 2742.92 secs

GenCore version 5.1.4_p5 4578
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 23:34:39 ; Search time 220.213 Seconds
(without alignments)
11770.723 Million cell updates/sec

Title: US-09-778-971-3
Perfect score: 1963
Sequence: 1 ggcgcagtgccggccat.....aaaaaaaaaaaaaaaaa 1963

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

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- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1472.2	75.0	2589	10	US-09-778-971-4
3	988.2	50.3	1841	10	US-09-886-404-17
4	983	50.1	1796	9	US-09-863-818A-1
5	980.8	50.0	1827	10	US-09-778-971-1
6	963.6	49.1	1515	9	US-09-874-503-11
7	963.6	49.1	1515	9	US-10-000-157-11
8	963.6	49.1	1515	9	US-10-063-547-157
9	963.6	49.1	1515	9	US-09-747-259-11
10	963.6	49.1	1515	9	US-10-176-590-399
11	963.6	49.1	1515	9	US-10-176-758-399
12	963.6	49.1	1515	9	US-10-063-616-157
13	963.6	49.1	1515	9	US-10-175-737-399
14	963.6	49.1	1515	9	US-10-063-502-157
15	963.6	49.1	1515	9	US-10-173-706-399
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17	963.6	49.1	1515	9	US-10-175-752-399
18	963.6	49.1	1515	9	US-10-176-482-399
19	963.6	49.1	1515	9	US-10-176-757-399

20	963.6	49.1	1515	9	US-10-176-913-399	Sequence 399, App
21	963.6	49.1	1515	9	US-10-180-552-399	Sequence 399, App
22	963.6	49.1	1515	9	US-10-180-557-399	Sequence 399, App
23	963.6	49.1	1515	9	US-10-173-700-399	Sequence 399, App
24	963.6	49.1	1515	9	US-10-174-572-399	Sequence 399, App
25	963.6	49.1	1515	9	US-10-174-579-399	Sequence 399, App
26	963.6	49.1	1515	9	US-10-174-582-399	Sequence 399, App
27	963.6	49.1	1515	9	US-10-174-588-399	Sequence 399, App
28	963.6	49.1	1515	9	US-10-175-739-399	Sequence 399, App
29	963.6	49.1	1515	9	US-10-175-740-399	Sequence 399, App
30	963.6	49.1	1515	9	US-10-175-743-399	Sequence 399, App
31	963.6	49.1	1515	9	US-10-176-488-399	Sequence 399, App
32	963.6	49.1	1515	9	US-10-176-492-399	Sequence 399, App
33	963.6	49.1	1515	9	US-10-176-747-399	Sequence 399, App
34	963.6	49.1	1515	9	US-10-176-750-399	Sequence 399, App
35	963.6	49.1	1515	9	US-10-176-985-399	Sequence 399, App
36	963.6	49.1	1515	9	US-10-176-987-399	Sequence 399, App
37	963.6	49.1	1515	9	US-10-176-991-399	Sequence 399, App
38	963.6	49.1	1515	9	US-10-176-992-399	Sequence 399, App
39	963.6	49.1	1515	9	US-10-176-993-399	Sequence 399, App
40	963.6	49.1	1515	9	US-10-184-658-399	Sequence 399, App
41	963.6	49.1	1515	9	US-10-173-695-399	Sequence 399, App
42	963.6	49.1	1515	9	US-10-173-697-399	Sequence 399, App
43	963.6	49.1	1515	9	US-10-173-705-399	Sequence 399, App
44	963.6	49.1	1515	9	US-10-174-576-399	Sequence 399, App
45	963.6	49.1	1515	9	US-10-174-585-399	Sequence 399, App

ALIGNMENTS

RESULT 1
US-09-778-971-3
; Sequence 3, Application US/09778971
; Patent No. US20020102639A1
; GENERAL INFORMATION:
; APPLICANT: Shaughnessy, John D.
; TITLE OF INVENTION: Evi27 Gene Sequence and Protein Encoded Thereby
; FILE REFERENCE: D6138
; CURRENT APPLICATION NUMBER: US/09/778,971
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/180,374
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 3
; LENGTH: 1963
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: prim transcript
; OTHER INFORMATION: cDNA of mouse Evi27
US-09-778-971-3

Query Match	100.0%	Score 1963;	DB 10;	Length 1963;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1963;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GTGGCCAGTGGCCGGCCCATGTTGCTAGTGTGCTGATCTTGGCTGCATCGTCAGGAGC	60	
Db	1	GTGGCCAGTGGCCGGCCCATGTTGCTAGTGTGCTGATCTTGGCTGCATCGTCAGGAGC	60	
Qy	61	GCCTTCGCTCGAGAGCCGCACTATTTCAGTGTGGCTCTGAGACAGGGCCCATCTCCAGAGTGG	120	
Db	61	GCCTTCGCTCGAGAGCCGCACTATTTCAGTGTGGCTCTGAGACAGGGCCCATCTCCAGAGTGG	120	
Qy	121	ATGGTCCAAACACACTCCTCCAGAGACTTGGAGGACCTCCAAAGTGGAACTCGTCAAG	180	
Db	121	ATGGTCCAAACACACTCCTCCAGAGACTTGGAGGACCTCCAAAGTGGAACTCGTCAAG	180	
Qy	181	ACAAAGTGTGGCAGCAGAGAGTGTTCATTTTGAATGAACATAGCTGGATATCTCCGGGCA	240	
Db	181	ACAAAGTGTGGCAGCAGAGAGTGTTCATTTTGAATGAACATAGCTGGATATCTCCGGGCA	240	

QY 241 GAGCCAGCATCCGCTGTTGTAAGGCCACCAAGATCTGGTGTAGTGGCAAAACCAACATG 300
 Db 241 GAGCCAGCATCCGCTGTTGTAAGGCCACCAAGATCTGGTGTAGTGGCAAAACCAACATG 300
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 Db 301 AATTTCATAGCTGTGTAGGTCGAATACACAGAGCCCTTCAAGCCGACAGACACCT 360
 QY 361 TCCGGGGGCAAAATGGACATCTCTATGTAGGCTTCCCTGTGAGCTGTAGCACTCTCTAT 420
 Db 361 TCCGGGGGCAAAATGGACATCTCTATGTAGGCTTCCCTGTGAGCTGTAGCACTCTCTAT 420
 QY 421 CTATCAGCGCCCAATACATCCCAATGTCTATATGAATGAGACAGCCCTTCTTTGTCT 480
 Db 421 CTATCAGCGCCCAATACATCCCAATGTCTATATGAATGAGACAGCCCTTCTTTGTCT 480
 QY 481 GTGAATCTTCACTCGCCAGGCTGCTTAACACAGTAAATGAATATATAAAGCGAGTCACT 540
 Db 481 GTGAATCTTCACTCGCCAGGCTGCTTAACACAGTAAATGAATATATAAAGCGAGTCACT 540
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 Db 541 GAGCGGGAAGCCTGTGGGACCCAGACATCACTGCTTGTAAAGAAACGAGAAGATGTT 600
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 Db 661 ACACATTTGGGTTTCTAGAGTCTGGAGATATAAATCTGATGAGGACGCTGTAGCCATC 720
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 Db 721 CCGGTGACTGAGGAGTGAAGTGGGTGTTTCACTGACCCCATATTTATCATACCTGC 780
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 Db 781 GGCATGACTGATCCGACGAGGAGGACAGTTGTCTTGTCTGAGACAAAGTGTCTCC 840
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 Db 841 ATCCCTCCAGATGACAAAGATGCTGGAGGCTGGCTGCTCTTCTTCTGTGTGCTG 900
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 Db 961 ACGAAGACGCTCTTCTTCTATTTCCACCATGCTCTGCTGCCCTCATTAAAGTCTGGTGT 1020
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 Db 1021 TATCCTTCTGAGATATGTTTCATACACCGTCTGTGGTTCACGTCTTCTTCTTCAAAAC 1080
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 Db 1081 TACTGCAAGTGTAGTCTATCTTGAATAATGCGAGAAAGAAATCGCCAGATGGG 1140
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 Db 1141 CCGGTACAGTGGCTGACCACTCAGAGCAAGCGGAGATAAAGTGTCTTCTTCTTCTTCC 1200
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Db 1321 ACGCATCTGCAAAATACCTGGTGTCTATCTTGGGGAGCAGACCTCAAGGGCGACTAT 1380
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 Db 1381 AATGCCCTGAGTGTCTGCCCAATATCATCTCATGAGGAGCGCCACAGCTTTCACACA 1440
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 Db 1441 GAACTTCTCAAGGCTACCGAGAGCATGTCAAGTGAAGAAACGCTCAAGAGCTGCCATGAT 1500
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 Db 1501 AGCTTCTCACCTTGTAGTCCACCGGGGGAATAGAGACTCTGAAGCCTTCTACTCTCC 1560
 QY 1561 CTTCCAGTGACAAATGTCTGTGAGCACTCTGAATGTGTGGGAGAGCTGTGTGGAGGT 1620
 Db 1561 CTTCCAGTGACAAATGTCTGTGAGCACTCTGAATGTGTGGGAGAGCTGTGTGGAGGT 1620
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 Db 1621 AGTGTATGTACAACTTGTCTTAAACTGGAGTTTGCAGAGTCAACCTGAGCATACAG 1680
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 Db 1681 CTTGAGGCTAGTCTATGCTGGATTTTAAAGACAAACAGTTTACAGCAATATAGTGTG 1740
 QY 1741 GGACCTACATTTGGGATATACCGCACTTCCAAAGCTGGGTAAATGATTTATCTGAGAACCCAGCACT 1800
 Db 1741 GGACCTACATTTGGGATATACCGCACTTCCAAAGCTGGGTAAATGATTTATCTGAGAACCCAGCACT 1800
 QY 1801 CTGGCCATGAAGTAAATACCGCACTTCCCTGTGAGCTCTGTGAGGTTGGTCTGTCTT 1860
 Db 1801 CTGGCCATGAAGTAAATACCGCACTTCCCTGTGAGCTCTGTGAGGTTGGTCTGTCTT 1860
 QY 1861 GCACCTGCCATGCTCTATGCTGACGTAGACCGTTTGTAAACATTTTAACTGTTTAAATGA 1920
 Db 1861 GCACCTGCCATGCTCTATGCTGACGTAGACCGTTTGTAAACATTTTAACTGTTTAAATGA 1920
 QY 1921 ATAATCCGTTTGGAGCTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1963
 Db 1921 ATAATCCGTTTGGAGCTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1963

RESULT 2

US-09-778-971-4
 ; Sequence 4, Application US/09778971
 ; Patent No. US20020102639A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shaughnessy, John D.
 ; TITLE OF INVENTION: Ev127 Gene Sequence and Protein Encoded Thereby
 ; FILE REFERENCE: D6138
 ; CURRENT APPLICATION NUMBER: US/09/778,971
 ; CURRENT FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: US 60/180,374
 ; PRIOR FILING DATE: 2000-02-04
 ; NUMBER OF SEQ ID NOS: 9
 ; SEQ ID NO 4
 ; LENGTH: 2589
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; NAME/KEY: prim transcript
 ; OTHER INFORMATION: cDNA of mouse Ev127
 US-09-778-971-4

Query Match 75.0%; Score 1472.2; DB 10; Length 2589;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1474; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 487 TTCACCTCGCCAGGCTGCTGCTTAAACCAAGTAAATGAATATAAAGAGCAGTGCAGGCG 546
 Db 1113 TTCACATTTCCAGGCTGCTGCTTAAACCAAGTAAATGAATATAAAGAGCAGTGCAGGCG 1172

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QY 547 GGAAGCCTGTGGGACCGAGACATCATCTGCTTGTAAAGAAACGAGAGATGGTTGAAGTG 606
DB 1173 GGAAGCCTGTGGGACCGAGACATCATCTGCTTGTAAAGAAACGAGAGATGGTTGAAGTG 1232
QY 607 AATTTTCAACCAATCCCTTTGGAAACAGATACAGGATTCCTATTCAACGGGACAGACA 666
DB 1233 AATTTTCAACCAATCCCTTTGGAAACAGATACAGGATTCCTATTCAACGGGACAGACA 1292
QY 667 TTGGGGTTTTCTAGAGTGTGGAGATAAATCTGATGAGGACGCTGTGATGACATCCCGGTG 726
DB 1293 TTGGGGTTTTCTAGAGTGTGGAGATAAATCTGATGAGGACGCTGTGATGACATCCCGGTG 1352
QY 727 ACTGAGAGAGTGAAGTGGGTGGTTTCAAGTGAACCCCATATTTATACATCTCGGGCAAT 786
DB 1353 ACTGAGAGAGTGAAGTGGGTGGTTTCAAGTGAACCCCATATTTATACATCTCGGGCAAT 1412
QY 787 GACTGATCCGACGCGAAGGACAGTTGTCTTGTCTGCTCAGAGCAAGTGTCTCCATCCCT 846
DB 1413 GACTGATCCGACGCGAAGGACAGTTGTCTTGTCTGCTCAGAGCAAGTGTCTCCATCCCT 1472
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DB 1473 CCAGATGACAAACAGACGATGCTGGGAGGCTGGCTGCTCTCTTCTGCTGCTGCTGGTG 1532
QY 907 GCTGTGTGGTGTGGGAGCTGGGATCTACTAACTTTGGAGGCAAGGAGGACAGAG 966
DB 1533 GCTGTGTGGTGTGGGAGCTGGGATCTACTAACTTTGGAGGCAAGGAGGACAGAG 1592
QY 967 ACCTGCTTCTTCTTATTTCCACCATGCTCCCTGCTCTTCTTCTTCTGCTGCTGCTTCTCT 1026
DB 1593 ACCTGCTTCTTCTTATTTCCACCATGCTCCCTGCTCTTCTTCTTCTGCTGCTGCTTCTCT 1652
QY 1027 TCTGAGATATGTTTCCATCACACCGCTGTGCTGCTTCACTGACTTTCTTCAAACTACTGC 1086
DB 1653 TCTGAGATATGTTTCCATCACACCGCTGTGCTGCTTCACTGACTTTCTTCAAACTACTGC 1712
QY 1087 AGAAGTGAAGTATCTTTGAAATAATGGCAGAAAAAGAAAAATGCCGAGATGGGCGCGTA 1146
DB 1713 AGAAGTGAAGTATCTTTGAAATAATGGCAGAAAAAGAAAAATGCCGAGATGGGCGCGTA 1772
QY 1147 CAGTGGCTGACCACTCAGAGCAAGCGGAGATAAAGTGTCTTCTTCTTCTTCTTCTTCTTCT 1206
DB 1773 CAGTGGCTGACCACTCAGAGCAAGCGGAGATAAAGTGTCTTCTTCTTCTTCTTCTTCTTCT 1832
QY 1207 GTCCCGACCTTTGTGACAGTGTCTGTGGCCCAATGAGGGCAGCGCAGGGAGAACTCT 1266
DB 1833 GTCCCGACCTTTGTGACAGTGTCTGTGGCCCAATGAGGGCAGCGCAGGGAGAACTCT 1892
QY 1267 CAGGATCTGTTCCTCTTGTCTTTAACTCTTTTGTAGTGAATTCAGACCCAGACGCAAT 1326
DB 1893 CAGGATCTGTTCCTCTTGTCTTTAACTCTTTTGTAGTGAATTCAGACCCAGACGCAAT 1952
QY 1327 CTGCAAAATACCTGTGTCTTCTTGGGGAGCAGACTTCAAGGCGACTATATGCC 1386
DB 1953 CTGCAAAATACCTGTGTGTCTTCTTGGGGAGCAGACTTCAAGGCGACTATATATGCC 2012
QY 1387 CTGAGTGTCTGCCCCCAATATCTCTCATGAAGGACCCACAGCTTTCCACACAGAACTT 1446
DB 2013 CTGAGTGTCTGCCCCCAATATCTCTCATGAAGGACCCACAGCTTTCCACACAGAACTT 2072
QY 1447 CTCAGGCTACGACAGCATGTCTGAGTGAAGAAACGCTTCAAGGCTGCCATGATAGTGT 1506
DB 2073 CTCAGGCTACGACAGCATGTCTGAGTGAAGAAACGCTTCAAGGCTGCCATGATAGTGT 2132
QY 1507 TCACCCCTTGTAGTCCACCGGGGGAATAGAGCTCTGAGACCTTCTTCTTCTTCTTCTTCTTCA 1566
DB 2133 TCACCCCTTGTAGTCCACCGGGGGAATAGAGCTCTGAGACCTTCTTCTTCTTCTTCTTCTTCA 2192
QY 1567 GTGACAAATGCTGTGTGACGACTCTGAAATGTGTGGGAGGCTGTGTGGAGGTAGTGTCT 1626
DB 2193 GTGACAAATGCTGTGTGACGACTCTGAAATGTGTGGGAGGCTGTGTGGAGGTAGTGTCT 2252
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QY 1627 ATGTACAAACTTGTCTTTAAAACTGGAGTTTGCAAGTCAACCTGAGCATACACGCTGAG 1686
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DB 2373 ACATTTGGGATATACCCAAAGCTGGGTAAATGATTATCACTGAGAACCCAGCACTCTGGCC 2432
QY 1807 ATGAAGTAATACGGCACTTCCCTGTCAGGCTGTCTGTAGGTTGGTCTGTCTTGTGCACTG 1866
DB 2433 ATGAAGTAATACGGCACTTCCCTGTCAGGCTGTCTGTAGGTTGGTCTGTCTTGTGCACTG 2492
QY 1867 CCATGCTCTATGCTGTCAGTACGACCGTTTGTAAACATTTTAACTGTTAAATGAATAATC 1926
DB 2493 CCATGCTCTATGCTGTCAGTACGACCGTTTGTAAACATTTTAACTGTTAAATGAATAATC 2552
QY 1927 CGTTTGGGAGCTCTCAAAAAAATAAAAAA 1963
DB 2553 CGTTTGGGAGCTCTCAAAAAAATAAAAAA 2589

RESULT 3
US-09-886-404-17
; Sequence 17, Application US/09886404
; Patent No. US20020037524A1
; GENERAL INFORMATION:
; APPLICANT: Medlock, Eugene
; APPLICANT: Yeh, Richard
; APPLICANT: Silbiger, Scott M.
; APPLICANT: Elliot, Gary S.
; APPLICANT: Nguyen, Hung O.
; APPLICANT: Jing, Shujian
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/37128B
; CURRENT APPLICATION NUMBER: US/09/886,404
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/810,384
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/266,159
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,125
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(1555)
US-09-886-404-17
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Query Match 50.3%; Score 988.2; DB 10; Length 1841;
Best Local Similarity 77.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 338; Indels 17; Gaps 4;
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QY 6 CAGTGGCCGGGCGCATGTGCTAGTGTGCTGATCTTGGCTGTCATCGTCAGGAGCGCCCT 65
DB 37 CAGTGGCCGGGCGCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 96
QY 66 GCCTCGAGAGCGCATATTCAGTGTGGCTCTGAGACAGGGCCATCTCCAGAGTGAATGT 125
DB 97 ACCCGGAGAGCGCATCGCTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGAATGT 156
QY 126 CCAACACACACTCACTCCAGGAGACTTGGGACCTCCAGTGGAACTCGTCAAGACAG 185
DB 157 ACAACATGATCTAATCCCGGAGACTTGGGAGCCTCCGAGTAGAACCTGTATTCAACATAG 216
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QY 186 TGTGGGAGCAGAGAGTTTCAATTTTGTATGAACATAAGCTGATCTCCGGCAGACGC 245
 DB 217 TGTGCAACAGAGGAGCTATTCAATTTTGTATGAATGAAGCTGGTACTCCGGCAGATGC 276
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 DB 277 CAGCATCCGCTCTTGAAGCCACCAAGATTTGTGTGAGCGGCAAAAGCAACTTCCAGTC 336
 QY 306 ATACAGCTGTGTGAGGTGCAATCTACACAGAGGCTTCCAAAGCCAGACAGACCTTCCGG 365
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 QY 366 CGCAAAATGACATCTCTATAGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCAT 425
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 QY 717 CATCCCGGTGACTGAGGAGTGAAGTGGGTGTTGAGCTGACCCCATATTTTACATAC 776
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 QY 837 TCCATCTCTCAGATGACAAACAGACGCTGCTGGAGGCTGCTGCTCTCTCTCTGT 896
 DB 877 CCTTTCTCTGATTAACAAACAGACGCGGAGGCTGCTGCTCTCTCTCTCTCT 936
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 DB 937 GTCTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGGATCTATCTAATGTGGAGGACGA 996
 QY 954 AAGGACGAGAGAGCTCTTCTTATTTTCCACATGCTCTGCTGCTCTCTTAAAGTCTCT 1013
 DB 997 AAGGATCAAGAAGACTTCTCTTTCTA- - -CCACACACTACTGCTGCTGCTTAAAGTCTCT 1053
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 QY 1074 TCAAACTACTGCAAGTGTGAGTCTATCTTGAATAATGGCAAAAGAAATAATCGCGA 1133
 DB 1114 TCAAAACCATTCGAAAGTGTGAGTCTATCTCGAAAGTGGCAAAAGAAATAATAGCAGA 1173
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 DB 1174 GATGGGTCCAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1233
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DB 1294 CAGTGAGAACTCTCAGACCTTCTCCCTTTCCTTTAACTTTTCTGCGTGTATTAAG 1353
 QY 1314 CAGCCAGAGGATCTGCACAAATACCTGCTGTCTATCTTGGGGAGCAGACCTCAAGG 1373
 DB 1354 AAGCCAGATTTCAATGCAAAATACGTTGGTGTCTACTTTAGAGATTTGATACAAAGA 1413
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 US-09-863-818A-1
 ; Sequence 1, Application US/09863818A
 ; Publication No. US20030092881A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorman, Daniel M.
 ; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
 ; FILE REFERENCE: DX01170K
 ; CURRENT APPLICATION NUMBER: US/09/863,818A
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/206,862
 ; PRIOR FILING DATE: 2000-05-24
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 1796
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (4)..(1509)
 ; OTHER INFORMATION:
 ; NAME/KEY: mat_peptide
 ; LOCATION: (46)..()
 ; OTHER INFORMATION:
 US-09-863-818A-1
 Query Match 50.1%; Score 983; DB 9; Length 1796;
 Best Local Similarity 77.9%; Pred. No. 0;
 Matches 1241; Conservative 0; Mismatches 335; Indels 17; Gaps 4;
 QY 16 GCCATGTTGCTAGTGTGCTCATCTTGGCTCATCTGTCAGAGCGCCCTGCTCGAGAG 75
 DB 1 GCGATGCTGCTGCTGCTTAAGCTTGGCGGCTGTGTCAGAGCGCGTACCCCGAGAG 60
 QY 76 CCGACTATTAGTGTGCTCTGACACAGGCGCATCTCCAGAGTGGATGGTCCAAACACA 135
 DB 61 CCGACCGTTCAATGTGCTCTGAAACTGGGCACTCTCCAGAGTGGATGTCTACACATGAT 120
 QY 136 CTCATCCAGAGACTTGAAGGACCTCCAGTGAACCTGTCAGACAGAGTGTGGCAGA 195
 DB 121 CTAATCCGGAGACTTGAAGGACCTCCAGTGAACCTGTTAACAATAGTGTGCAACA 180
 QY 196 CAGGAGTTTCAATTTTATGAACATAAGCTGGATATCTCCGGGAGAGCGCCAGATCCGC 255
 DB 181 GGGACTATTCAATTTTATGAATGTAAAGTGGTACTCCGGGAGAGTCCAGCATCCGC 240
 QY 256 TTGTGAAGGCCCAAGATCTCGTGTGAGTGGCAAAACAAACATGAATTTCAATAGCTGT 315

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Db 241 TTGTTGAAGGCCACCAAGATTGTTGTCGCGGCAAAAGCAACTTCAGTCTCAGCTGT 300
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Db 301 GTGAGGTGCAATTAACACAGAGGCTTCCAGACTCAGACACAGACCTCTGGTGTAAATGG 360
QY 376 ACATTCCTCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCATCAGCGCCAT 435
Db 361 ACATTTCTCTATATCGGCTTCCCTGTAGAGCTGAACACAGCTATTTCATTTGGGGCCCAT 420
QY 436 AACATCCCAATCTAATATGAATGAGGACAGCCCTTCTTTGCTGTGAACCTTCACTCG 495
Db 421 AATATTTCTAATGCAATATGATGAGATGGCCCTTCCATGCTGTGAATTTCACTCA 480
QY 496 CCAGGTGCTTAAACCAACGCTAATGAATATAAAGACAGTGCACTCAGCGCGGAACCTG 555
Db 481 CCAGGTGCTGTAGACCACATATGAATATAAAGAAAGTGTCAAGGCGCGGAAGCTG 540
QY 556 TGGGACCCAGACATCACTGCTTTGTAAGAACGAGAGATGGTTGAAGTGAATTTTACA 615
Db 541 TGGGATCCGAACATCACTGCTTTGTAAGAAAGATGAGGAGACAGTAGAAGTGAACTTACA 600
QY 616 ACCAATCCCTTGGAAACAGATACAGATTCTCATTTCAACGGGACACGACATTGGGGTTT 675
Db 601 ACCATCCCTTGGAAACAGATACATGGCTCTTATCCAAACAGCACTATCATCGGGTTT 660
QY 676 TCTAGAGTCTGG-----AGATAAATCTGATGAGGACGCTCTAGCCATCCCGGTG 726
Db 661 TCTCAGGTGTTTGAGCCACACAGAGAAACAAACGCGAGCTTCAGTGGTATTCCAGTG 720
QY 727 ACTGAGGAGTGAAGGTGGGTGGTTTACGTGACCCCATATTTATCATACCTGCGGCAAT 786
Db 721 ACTGGGGATGATGAAGGTGCTACGCTGCAGCTGACTCCATATTTCTTCTACTTGTGGCAGC 780
QY 787 GACTGCATCCGACGCAAGGGACAGTTGCTTTGCTTCAGAGCAAGTGTCTCCATCCCT 846
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QY 847 CCAGATGACAACAGACGATGCTGGAGGCTGGCTGCCTCTCTCTCTCTCTCTCTCTCTCTG 903
Db 841 CTGGATAACAACAAGAACGCGGAGGCTGGCTGCCTCTCTCTCTCTCTCTCTCTCTCTCTG 900
QY 904 GTGGCTGTGGGTGCTGGAGCTGGGATCTACCTAACTTGGAGGCAAGGAGGACAG 963
Db 901 GTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCAAGGAGGATCAAG 960
QY 964 AAGAGCTCTCTTCTTCTATTTCCACATGCTCTGCGAGGCTGGCTGCCTCTCTCTCTCTCTCT 1023
Db 961 AAGACTCTCTCTTCTA---CCACCACTACTGCCCCCCTAATTAAGGTCTTGTGGTTTAC 1017
QY 1024 CCTTCTGAGATATGTTTCCATCACACCGCTCTGTGCTTCACTGACTTTCTTCAAAACTAC 1083
Db 1018 CCATCTGAATATGTTTCCATCACAAATTTGTACTTCACTGAATTTCTTCAAAACCAT 1077
QY 1084 TGCAGAAGTGAGTGTATCTTGAATAATGGCAGAAAAAGAAATCCCGAGATGGGGCGG 1143
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QY 1204 GACGTCCCGACCTTTGTGACAGTGCCTGTGGCCACAATAGAGGCGCAGCGCAGGAGAAC 1263
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QY 1264 TCTCAGGATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1323
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QY 1444 CTTCTCAAGGCTACGACAGCATGTCTGAGAAACGCTCACAAGCCCTGCCATGATAGC 1503
Db 1438 CTTCTCCATGTCAAGCAGCAGGTGTCTCAGGAGAAAGATCACAGCCCTGCCACGATGC 1497
QY 1504 TGTTCACCCCTTCTAGTCCACCGGGGAA--TAGAGACTCTCTGAAGCCTTCTCTACTCTCC 1561
Db 1498 TGCTGCTCTCTGTAGCCACCCCATGAGAGCAGAGACCTTAAGGCTTCTCTATCCACC 1557
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Db 1558 AATTACAGGAAAAAACAAGTGTGATGATCCTGAA 1590
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; APPLICANT: Shaughnessy, John D.
; TITLE OF INVENTION: Evi27 Gene Sequence and Protein Encoded Thereby
; FILE REFERENCE: D6138
; CURRENT APPLICATION NUMBER: US/09/778,971
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/180,374
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 1
; LENGTH: 1827
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: prim transcript
; OTHER INFORMATION: cDNA of human Evi27
US-09-778-971-1
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Query Match 50.0%; Score 980.8; DB 10; Length 1827;
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Matches 1240; Conservative 0; Mismatches 337; Indels 17; Gaps 4;
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Db 62 GCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAAATGA 121
QY 135 ACTCACTCCAGAGACTTGAGGAGCTCCAGTGGAACTCGTCAAGACAAGTGTGGCAGC 194
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QY 375 GACATTTCTCTATGTAGGCTTCCCTGTGTGAGTGTGAGCACTCTCTATCTCATCAGCGCCCA 434
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QY 435 TAACATCCCAATGCTAATATGAATGAGGACAGCCCTTCTTTGTCTGTGAACCTTCACTCTC 494
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; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
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; PRIOR FILING DATE: 2000-08-24
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; PRIOR FILING DATE: 2000-06-02
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; PRIOR APPLICATION NUMBER: US PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 11
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-874-503-11

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Query Match      49.1%; Score 963.6; DB 9; Length 1515;
Best Local Similarity 78.7%; Pred. No. 36-313;
Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;

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QY 73 GAGCCGACTATTCAAGTGTGGCTCTGAGACAGGCGCATCTCCAGATGGATGGTCCAAAC 132
DB 61 GAGCCGACCGTTCAATGTGGCTCTGAACTGGGCAATCTCCAGATGGATGGTCCAAAC 120
QY 133 ACATCACTCCAGGAGACTTGGAGGAGCTCCAAAGTGGAACTGCTCAAGACAAAGTGGCA 192
DB 121 GATCTAATCCCGGAGACTTGGAGGAGCTCCGAGTAGAACCTGTTACAACTAGTGTGCA 180
QY 193 GCAGAGGAGTTTCAATTTTGTATGACATAAGCTGATCTCGGGCAGACGCCCATC 252
DB 181 ACAGGGGAGCTATTCAATTTTGTATGAACTGAACTGGGTACTCCGGCAGATGCCAGCATC 240
QY 253 CGCTTCTTGAAGGCCACCAAGACTCTGGTGTAGTGGCAAAACAAATGATGAATTCATACAGC 312
DB 241 CGCTTGTGAGGCCACCAAGATTGTGTGACCGGCAAAAGCACTTCAGTCTCTACAGC 300
QY 313 TGTGTAGGTGCAACTACACAGAGGCTTTCCAAAGCCAGACAGACCTTCCCGGCGCAAA 372
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QY 373 TGGACATTTCTCTATGAGGCTTCCCTGTGGAGCTGAGCACTCTATCTCATFACAGCGCC 432
DB 361 TGGACATTTCTCTATGAGGCTTCCCTGTGGAGCTGAGCACTCTATCTCATFACAGCGCC 420
QY 433 CATACATCCCAATGCTAATGATGAGGACAGCCCTCTTTGCTGTGAACTTCACC 492
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QY 493 TCGCCAGGCTGCTTAAACCAACGTAATGAAATATAAAAGCAGTGCACTGAGGCGGGAAGC 552

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DB 481 TCACCAAGGCTGCTAGACCACATAATGAAATATAAAAAAAGTGTCTCAAGGCGCGAAGC 540
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QY 724 GTGACTGAGGAGAGTGAAGGTGGTGTTCAGCTGACGCCCATATTTATCATACCTCTCGGC 783
DB 721 GTGACTGGGATGATGAAGGTGCTACGGTGCAGTCACTCCATATTTTCTACTTGTGSC 780
QY 784 AATGACTGCATCCGACGCGAAGGACAGTTGTCTTTGTCTCAGAGACAAAGTGTCTCCATC 843
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QY 844 CCTCCAGATGACAAACAGACGATGCTGGAGGCTGCTGCTCTCTCTCTGTTG---CTG 900
DB 841 CCTCTGGATAACAAACAAAGCAAGCGGAGGCTGGCTGCTCTCTCTCTGTTGCTCTG 900
QY 901 CTGGTGGCTGTGTGGTGTCTGCGAGCTGCGAGCTGCTGAGGAGCTGCTCTCTCTGTTG 960
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QY 1501 AGCTGTTCACTCTGTAG 1518
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US-10-000-157-11
; Sequence 11, Application US/10000157
; Publication No. US20020182673A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul L.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovaanik, Melissa.
; APPLICANT: Vanlookeren, Menno
; APPLICANT: Vandien, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381C1P4 (US)
; CURRENT APPLICATION NUMBER: US/10/000,157
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/138387
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; PRIOR APPLICATION NUMBER: 09/874503
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; PRIOR APPLICATION NUMBER: 09/908827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/931836
; PRIOR FILING DATE: 2001-08-16
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; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
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; PRIOR FILING DATE: 2000-03-21
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; PRIOR APPLICATION NUMBER: PCT/US00/23328
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; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
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; PRIOR FILING DATE: 2001-06-01
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; PRIOR FILING DATE: 2001-06-20
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; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 11
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-000-157-11

Query Match 49.1%; Score 963.6; DB 9; Length 1515;
Best Local Similarity 78.7%; Pred. No. 3e-313;
Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;

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Qy	73	GAGCGGACTATTTCAGTGTGGCTCTGAGACAGGCGCATCTCCAGAGTGGATGGTCCAAAC	132
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Qy	133	ACATCTACTCCAGGAGACTTGAGGAGCTCCAAAGTGGAACTCTCGACAGACAAGTGTGCA	192
Db	121	GATCTAATCCCGGAGACTTGAGGAGCTCCGAGTAGAACCTGTTACAACTAGTGTGCA	180
Qy	193	GCAGAGGAGTTCATTTGATGAACATAGCTGGATCTCCGGGAGAGCGCAGCATC	252
Db	181	ACAGGAGACTTTCATTTGATGAACATAGCTGGATCTCCGGGAGAGCGCAGCATC	240
Qy	253	CGCTTGTGAAGGCCACCAAGATCTGCGTGAAGTGGCAAAAAACAACATGAATTCATACAGC	312
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Qy	313	TGTGTAGGTGCAACTACACAGAGGCGCTTCCAAAGCCAGACCACTTCCGGGGGCAAA	372
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RESULT 9

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US-09-747-259-11
; Sequence 11, Application US/09747259
; Publication No. US20030008815A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1 (US)
; CURRENT APPLICATION NUMBER: US/09747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
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; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 11
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-747-259-11

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Query Match 49.1%; Score 963.6; DB 9; Length 1515;
 Best Local Similarity 78.7%; Pred. No. 3e-313;
 Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;

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Qy 13 CGGGCGATGTTGCTAGTGTCTGCTGATCTTGGCTGCTGATCGTCAGAGCGGCTGCTCGA 72
Db 1 CGGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Qy 73 GAGCGGACTATTTCAGTGTGGCTCTTGAGACAGGGCCATCTCCAGAGTGGATGGTCCACAC 132

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Db	1138	CCAGTGGAGTGGCTTGCCTCACTCAAAAGAAGGCGACAGACAAAGTCGTCTCTCTCTTTCC	1139
Qy	1201	AGTGAGCTCCCGACCCCTTTTGTGACAGTGCCTGTGGCCCAATAGAGGCGACGCCAGGGAG	1260
Db	1198	AATGAGCTCAACAGAGTGTGTGCGATGATACCTGTGSCAAGAGCGAGGCGAGTCCCAGTGAG	1257
Qy	1261	AACCTCTCAGGATCTGTTCCCTCTTGCCCTTTAACTCTTTTGTAGTGATTTTCAGCAGCCAG	1320
Db	1258	AACCTCTCAAGACCTCTTCCCTCTTGCCCTTTAACTCTTTTCTGCAGTGATCTAAGAAGCCAG	1317
Qy	1321	ACGCATCTGCACAAATACCTGCTGTGTCTATCTTGGGGGAGCAGACCTCAAAAGGCGACTAT	1380
Db	1318	ATTTCATCTGCAAAATACGTGTGTGTCTACTTTAGAGAGATTGATACAAAGAGCATTTAC	1377
Qy	1381	AATGCCCTCAGTGTCTGCCCCCAATATCATCTCATGAAGAGCGCACAGCTTTTCCACACA	1440
Db	1378	AATGCTCTCAGTGTCTGCCCCCAAGTACCACCTCATGAAGGATGCCACTGTCTTCTGTGCA	1437
Qy	1441	GAACCTTCTCAGGCTACGCGAGAGCATGTCTAGTGAAGAAACCTCACAAGCCTTGCCTGAT	1500
Db	1438	GAACCTTCTTCATGTCTCAAGCAGCAGGCTGTCTCAGCAGGAAAAAGATCACAAGCCTGCCAGAT	1497
Qy	1501	AGCTGTTTACCCTTTGTAG	1518
Db	1498	GGCTGCTCTCCTTTGTAG	1515
RESULT 10			
US-10-174-590-399			
; Sequence 399, Application US/10174590			
; Publication No. US20030008352A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Chen, Jian			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Pan, James			
; APPLICANT: Smith, Victoria			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Wood, William I.			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; FILE OF INVENTION: ACIDS ENCODING THE SAME			
; FILE REFERENCE: P3430R1C42			
; CURRENT APPLICATION NUMBER: US/10/174,590			
; CURRENT FILING DATE: 2002-06-18			
; Prior application removed - See File Wrapper or Palm			
; NUMBER OF SEQ ID NOS: 612			
; SEQ ID NO 399			
; LENGTH: 1515			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
US-10-174-590-399			
Query Match 49.1%; Score 963.6; DB 9; Length 1515;			
Best Local Similarity 78.7%; Pred. No. 3e-313;			
Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps			
Qy	13	CGGGCCATGTTGTAGTGTGTCTGATCTTTGGCTGCATCGTGCAGGAGCGCCCTGCCTCGA	72
Db	1	CCGGCGATGTCGTCGTCTGCTAGCTTGGCCGGCTGTGCAGGAGCGCGTACCCCGA	60
Qy	73	GAGCGCAGTATTTCAGTGTGGCTCTGAGACAGGGCCATCTCCAGAGTGATGTGTTCAACAC	132
Db	61	GAGCGCAGCGTTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGTCTACAAAT	120
Qy	133	ACACTCCTCCAGGAGACTTGAGGACCTCCAAAGTGGAACTCGTCAAGACAAGTGTGGCA	192
Db	121	GATCTAATCCCGGAGACTTGAGGACCTCCAGTAGAACTGTTCACACTAGTGTGTGCA	180
Qy	193	GCAGAGGAGTGTTCATTTTGTATGAACATAAGCTGGATCTCTCCGGGCGAGCGCCAGCATC	252

Db 181 ACAGGGGACTATTCAATTTTGTGATGTAAGCTGGGTACTCGGCGAGATGCCAGCATC 240
 Qy 253 CGCTTGTGAGGCGCCACCAAGATCTCGGTGAGTGGCAAAACAAAGATGAATTCATACAGC 312
 Db 241 CGCTTGTGAGGCGCCACCAAGATTTGTGTGACGGGCAAAAGCAATTCAGTCTCTACAGC 300
 Qy 313 TGTGTGAGGTGCAACTACACAGAGGCGCTTCCAAAGCCAGACACAGACTTCCGGCGGCAAA 372
 Db 301 TGTGTGAGGTGCAATACACAGAGGCGCTTCCAGACTCAGACACAGACCCCTCTGGTGTAA 360
 Qy 373 TGAACATCTCTATGATGAGGCTTCCGTGTGAGCTGAGCACTCTATCTCATACAGCGCC 432
 Db 361 TGAACATCTCTATGATGAGGCTTCCGTGTGAGCTGAGCACTCTATCTCATACAGCGCC 420
 Qy 433 CATAACATCCCAATGCTAATATGAATGAGGACAGCGCTTCTTGTCTGTGACTTCACC 492
 Db 421 CATAATATCTAATGCAAAATGAATGAAGATGGGCGCTTCCATGTCTGTAATTTTACC 480
 Qy 493 TCGCCAGGCTGCCTAAACACAGCTAATGAATATAAAAGCAGTGCACTGAGGCGGGAAGC 552
 Db 481 TCACCAGGCTGCCTAGCCACATATGAATATAAAAGTGTCTCAAGCGCGGAAGC 540
 Qy 553 CTGTGGAGCCAGACATCACTCTTTGTAAGAAAGAGAGATGTTGAAAGTGAATTC 612
 Db 541 CTGTGGAGCCGAAACATCACTCTTTGTAAGAAAGAGAGATGTTGAAAGTGAATTC 600
 Qy 613 ACAACCAATCCCTTGGAAACAGATACAGATCTCTATTCACGGGACAGCATTTGGG 672
 Db 601 ACAACCACTCCCTTGGAAACAGATACAGATCTCTATTCACAGCACTATCATCGGG 660
 Qy 673 TTTTCTAGAGTGTGG-----AGATAAATCACTGAGGAGCTCTGTAGCCATCCCG 723
 Db 661 TTTTCTAGAGTGTGGAGCCACACAGAGAAACAAACCGAGCTTCAGTGTGATTCGA 720
 Qy 724 GTGACTGAGGAGATGAAGTGGGTGTTGAGTCACTGACCCCATATTTATCATACCTGCGGC 783
 Db 721 GTGACTGAGGAGATGAAGTGGGTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAG 780
 Qy 784 NATGACTGATCCGAGCGGAGGAGTGTGCTTTGCTGAGTCACTGAGTCACTGAGTCACTGAG 843
 Db 781 AGCGATGATCCGATCAATGAAGAAACAGTGTGCTCTGCGCCAAACAGGCGTCCCTTTC 840
 Qy 844 CTTCAGATGACAAACAGACGATGCTGGGAGGCTGCTGCTCTCTCTCTGCTGCTG---CTG 900
 Db 841 CCTCTGATTAACAAACAGACGCGGAGGCTGCTGCTCTCTCTCTGCTGCTGCTG 900
 Qy 901 CTGGTGGCTGTGTGGGTGTGGGAGTGTGAGTCTACCTAATCTGAGGCAAGGAAGGAGC 960
 Db 901 CTGGTGGCCACATGGGTGTGGTGGGAGGATCTATCTAATGTGGAGGCAAGGAAGGATC 960
 Qy 961 AGGAAGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020
 Db 961 AGGAAGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1017
 Qy 1021 TATCTCTTCTGAGATATGTTTCCATCACACCGTCTGTGCTTCTCACTGACTTCTTCTTCTTCT 1080
 Db 1018 TACCCATCTGAATATGTTTCCATCACAAATTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1077
 Qy 1081 TACTGAGAAGTGAAGTCTATCTTGAATAATGGCAAAAGAAATATCCCGAGATGGG 1140
 Db 1078 CATTGAGAAGTGAAGTCTATCTTGAATAATGGCAAAAGAAATATAGCAGATGGT 1137
 Qy 1141 CCGGTACAGTGTGCTGACCTCAGAGCAAGCGGAGATGAAGTGGTCTTCTTCTTCTTCTTCTTCT 1200
 Db 1138 CCAGTGTGAGTGTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1197
 Qy 1201 AGTGAGTCTCCGACCTTGTGACAGTGTCTGTGGCCAAATGAGGCGAGCGCCAGGAG 1260
 Db 1198 NATGAGTCAACAGTGTGTGCGATGTGATCTGTGGCAGAGCGGCGAGTCCGAGTGA 1257
 Qy 1261 AACTCTCAGGATCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320

Db 1258 AACTCTCAGAGCTCTTCCCTTCCCTTTAACTTTTCTGAGTGAATCTAAGAAAGCCAG 1317
 Qy 1321 AGCATCTGCAAAATACCTGCTGTCTATCTTGGGGAGCAGACCTCAAGAGCGACTAT 1380
 Db 1318 ATTCACTGCAAAATACCTGCTGTCTATCTTGGGGAGCAGACCTCAAGAGCGACTAT 1377
 Qy 1381 AATGCCCTCAGTGTCTGCCCCCAATATCATCTCATGAAGGAGCGCCACAGCTTTCACACA 1440
 Db 1378 AATGCTCTCAGTGTCTGCCCCCAATATCATCTCATGAAGGAGCGCCACAGCTTTCACACA 1437
 Qy 1441 GAACTTCTCAAGGCTACGCGAGAGCATGTGAGTGAAGAAACGCTCACAAGCTTGCATGAT 1500
 Db 1438 GAACTTCTCAGTGTCTGCCCCCAATATCATCTCATGAAGGAGCGCCACAGCTTTCACACA 1497
 Qy 1501 AGCTGTTCCACCTTGTAG 1518
 Db 1498 GCTGCTCTCTCTTGTAG 1515

RESULT 11

US-10-176-758-399
 ; Sequence 399, Application US/10176758
 ; Publication No. US20030008353A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul. J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C104
 ; CURRENT APPLICATION NUMBER: US/10176,758
 ; CURRENT FILING DATE: 2002-06-21
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 399
 ; LENGTH: 1515
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-176-758-399

Query Match 49.1%; Score 963.6; DB 9; Length 1515;
 Best Local Similarity 78.7%; Pred. No. 3e-313;
 Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;

Qy 13 CGGGCCATGTTGCTAGTGTGCTGATCTTGGCTGATCTGTCAGAGGCGCCCTGCTGCA 72
 Db 1 CGGGCGATGTCGCTGCTGCTGCTAAGCTTGGCTGCTGTCAGAGGCGCGCTACCCCGA 60
 Qy 73 GAGCCGCTATTCTAGTGTGCTGTCAGAGGCGCCATCTCCAGAGTGGATGCTGCTCAACAC 132
 Db 61 GAGCCGCTGTTCAATGTGGCTCTGAACCTGGGCTCTCCAGAGTGGATGCTCAACAT 120
 Qy 133 ACATCTCACTCCAGAGACTTTCAGGAGCCTCCAGTGGAACTCTGCAAGACAAGTGTGGCA 192
 Db 121 GATCTAATCCCGAGACTTTCAGGAGCCTCCAGTGGAACTCTGCAAGACAAGTGTGGCA 180
 Qy 193 CGAGAGAGTGTTCATTTGATGAACATAGCTGGATATCTCCGGGAGAGCGGAGCATC 252
 Db 181 ACAGGGCACTATTCAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Qy 253 CGCTTGTGAGGCGCCACCAAGATCTGCTGAGTGGCAAAACAAACAAATGATTCATACAGC 312
 Db 241 CGCTTGTGAGGCGCCACCAAGATTTGTGACGGGCAAAAGCAACTTCCAGTCTCTACAGC 300
 Qy 313 TGTGTGAGGTGCAACTACAGAGGCGCTTCCAAAGCCAGACCGACTTCCGGCGGCAAA 372

Db 301 TGTGTGAGGTGCAATTACACAGAGGCTTCCAGACTCAGACGACCTCTGTGTGTAA 360
QY 373 TGGACATTTCTCTATGTAGGCTTCCCTGTGGAGTGGAGCTCTCTATCTCATCAGCGCC 432
Db 361 TGGACATTTCTCTATGTAGGCTTCCCTGTGGAGTGGAGCTCTATCTCATCAGCGCC 420
QY 433 CATACATCCCAATGCTAATATGAATAGGACAGCGCTTCTTTGTCTGTGAATCTCAC 492
Db 421 CATATATTTCTAATGCAATATGAATAGGATGGCGCTTCCATGTCTGTGAATTTCA 480
QY 493 TGGCAGGCTGCTTAACACACGTAATGAATATAAAGAGAGTGCAGTGGCGGAGC 552
Db 481 TACACAGGCTGCTTAGACACATAATGAATATAAAGAGAGTGTGTCAAGCGCGAAGC 540
QY 553 CTGTGGAGCCAGACATCACTGCTTGTAAAGAGAAAGAGAGAGTGTGAAGTGAATTC 612
Db 541 CTGTGGAGCCGAACATCACTGCTTGTNAGAAGAAAGAGAGACAGTGAAGTGAATTC 600
QY 613 ACACCAATCCCTTGGAAACAGATACAGATTTCTCATTCACGGGACAGCATTTGGGG 672
Db 601 ACACCACTCCCTTGGAAACAGATACATGCTCTTATCCAAACAGACACTATCATCGG 660
QY 673 TTTTCTAGAGTGTGG-----AGATAACTGATGAGGAGCTGTAGCCATCCG 723
Db 661 TTTTCTAGAGTGTGGAGCCACACAGAGAAACAAACGCGAGCTTCAAGTGTATCCA 720
QY 724 GTGACTGAGGAGTGAAGTGGGTGTTGAGTCACTGACCCCATATTTACATACCTCGGC 783
Db 721 GTGACTGGGGATGAGAGTGTACGGTGCAGCTGACTCATATTTTCTACTTGTGGC 780
QY 784 AATGACTGCATCCGACCGAAGGAGACAGTTGTCTTGTCTCAGAGACAAAGTGTCCCATC 843
Db 781 AGCGACTGCATCCGACATAAAGAGAAAGTGTCTGTGCCCAAAACAGCGCTCCCTTC 840
QY 844 CTCCAGATGACACAGACGATGCTGGAGAGGTGCTGCTCTCTCTCTGTGTG---CTG 900
Db 841 CCTCTGGATTAACAAACAAAGCAAGCGGAGGCTGGCTCTCTCTCTCTGTGTCTG 900
QY 901 CTGGTGGCTGTGGGTGCTGGGAGTGGGATCTACTTAAGTGGAGGCAAGAGGAGC 960
Db 901 CTGGTGGCCACATGGGTGCTGGGAGGAGGATCTATCTAATGTGGAGGACGAAAGATC 960
QY 961 AGAAGACTTCTTTCTA---CCACACACTACTGCCCGCCCATTAAGGTCTTGTGGTT 1017
Db 1021 TATCTCTGAGATATGTTTCCATCACCGTCTGTGGCTTCACTGACTTTCTTCAAAC 1080
QY 1018 TACCCATCTGAATATGTTTCCATCACAAATTTGTACTTCACTGAATTTCTTCAAAC 1077
QY 1081 TACTGAGAGTGAAGTGCATCTTGAATAATGGCAGAAAAGAAATCGCGAGATGGGG 1140
Db 1078 CATTGCAAGTGAAGTGCATCTTGAAGTGGCAGAAAAGAAATAGCAGAGTGGGT 1137
QY 1141 CCGGTACAGTGGCTGACCTCAGAGCAAGCGGAGATAAAGTGGTCTTCTTCTTCCC 1200
Db 1138 CCAGTGCAGTGGCTTCCCACTCAAAGAGAGGAGCAGACAAAGTCTCTTCTTCTTCC 1197
QY 1201 AGTACGTCGACCCCTTTGTGACAGTGGCTGTGGCCACAATGAGGCGAGCGCAGGAG 1260
Db 1198 AATGAGTCAACAGTGTGTGCGATGTGTCTGTGGCAGAGCGAGGCGAGTCCAGTGAG 1257
QY 1261 AACTCTCAGATCTGTCCCTCTTGCCTTTTAACTCTTTTGTAGTGAATTCAGCAGCCAG 1320
Db 1258 AACTCTCAGAGCTCTTCCCTCTTGCCTTTTAACTCTTTTGTAGTGAATTCAGCAGCCAG 1317
QY 1321 AGCATCTGCACAAATACCTGTGTGTCTATCTTGGGGAGCAGACCTCAAAGCGGACTAT 1380
Db 1318 ATTATCTGCACAAATACCTGTGTGTCTACTTTAGAGAGATTGATACAAAAGAGATTAC 1377
QY 1381 AATGCCCTGAGTGTCTGCCCAATATCATCTCATGAAGGAGCGCCACAGCTTTCACACA 1440

Db 1378 AATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGA 1437
QY 1441 GAATTTCTCAAGGCTACGACAGAGCATGTCAAGTGAAGAAACGCTCAAGAGCTGCCATGAT 1500
Db 1438 GAATTTCTCAAGTCAAGCAGCAGGCTGTCAAGAGAAAGATCAAGAGCTGCCAGAT 1497
QY 1501 AGCTGTTTCACTTGTAG 1518
Db 1498 GGCTGCTGCTCTTGTAG 1515
RESULT 12
US-10-063-616-157
; Sequence 157, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 157
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-157
Query Match 49.1%; Score 963.6; DB 9; Length 1515;
Best Local Similarity 78.7%; Pred. No. 3e-313;
Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;
QY 13 CGGGCCATTTCTAGTGTGTGCTGATCTTTGGTGCATCTGTGAGGAGCGCCCTGCTCTGA 72
Db 1 CGGGCGATGCTGCTGCTGCTGCTAAAGCTTGGCGCGCTGTGAGGAGCGCGTACCCCGA 60
QY 73 GAGCGCATTTTCACTGTGGCTCTGAGACAGCGGCATCTCCAGAGTGGATGTCNAACAC 132
Db 61 GAGCGACCGTTCATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACT 120
QY 133 ACACCTCACTCCAGGAGACTTGAAGGACCTCCAAAGTGGAACTCGTCAAGACAAGTGTGGCA 192
Db 121 GATCTAATCCCGGAGACTTGAAGGACCTCCGAGTAGAACCTGTTACAACCTAGTGTGA 180
QY 193 GCAGAGAGTGTTCATTTTGTATGAACATAAGCTGGATCTCCGGGAGACGCCAGCATC 252
Db 181 ACAGGGAGCTATTTCAATTTTGTATGAATGTAAGTGGTACTCCGGGAGATGCCAGCATC 240
QY 253 CGCTTGTGAAGGCGACCAAGATCTCGGTGAGTGGCAAAAACAAATGATGATATACAGC 312
Db 241 CGCTTGTGAAGGCGACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTTACAGC 300
QY 313 TGTGTGAGTGCACACTACACAGAGCGCTTCCAAAGCGAGACAGACCTTCCGGCGGCAAA 372
Db 301 TGTGTGAGTGCACACTTACACAGAGCGCTTCCAGACTCAGACAGACCTTCTGTGTGA 360
QY 373 TGGACATTTCTCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCATCAGCGCC 432
Db 361 TGGACATTTCTCTATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCAATTTGGGCC 420
QY 433 CATACATCCCAATGCTAATATGAATAGGACAGCGCTTCTTTGTCTGTGAATTTCAAC 492
Db 421 CATATATTTCTTAATGCAATATGAATAGGATGGCGCTTCCATGTCTGTGAATTTCAAC 480

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QY 493 TCGCCAGGCTGCCATAAACACAGTAATGAATATAAAAAAGCAGTGCACTGAGCGGGAAGC 552
Db 481 TCACCAAGGCTGCTAGACACACATAATGAATATAAAAAAGTGTCTCAGCGCGGAAGC 540
QY 553 CTGTGGGAGCCAGACATCACTGCTTTGTAAGAAAGACAGAGATGGTTGAAGTGAATTC 612
Db 541 CTGTGGGATCCGAACATCACTGCTTTGTAAGAAAGATGAGGAGACAGTAGAAGTGAATTC 600
QY 613 ACAACAAATCCCTTCGAACACAGATACAGATTCTCATTCACGGGACACAGCATTTGGG 672
Db 601 ACAACCACTCCCTTCGGAACACAGATACATGGCTCTTATCCACACAGCACTATCATCGGG 660
QY 673 TTTTCTAGAGTGTGCG-----AGATAAACTGATGAGGACGCTCTAGCCATCCCG 723
Db 661 TTTTCTCAGTGTGTTGAGCCACACACAGAGAAACAAACGCGACTTCACTGTGATTCCA 720
QY 724 GTGACTGAGGAGTGAAGTGGTGGTTCAGCTGACGCCCATATTTATCATACCTGCGGC 783
Db 721 GTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC 780
QY 784 AATGACTGCATCGGACGCAAGGACAGTTGTCTTTGCTCAGACAAAGTCTCCCATC 843
Db 781 AGCGACTGCATCCGACATAAAGGAACAGTTGTCTCTGCCCCAACACAGGCGTCCCTTTC 840
QY 844 CTCCAGATGACAAACAGACGATGCTGGGAGGCTGGCTCTCTTCTCTGTTG---CTG 900
Db 841 CTTCTGGATAAACAAACAGACGAGCGGAGGCTGGCTGCTCTCTCTGCTGTCTG 900
QY 901 CTGTGGCTGTGTGGTGTGTCAGCTGGGATCTACCTAACTTGGAGGCAAGGAAGGAGC 960
Db 901 CTGGTGGCCACATGGTGTCTGGTGGCAGGATCTATCTAATGGAGGCAACGAAGGATC 960
QY 961 ACGAGACGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020
Db 961 AAGAAGACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1017
QY 1021 TATCTTCTGAGATATGTTTTCATCACACCGTCTGTGCGCTTCACTGACTTTCTTCAAAAC 1080
Db 1018 TACCCATCTGAATATGTTTTCATCACAAATTTGTACTTCACTGAATTTCTTCAAAAC 1077
QY 1081 TACTGAGAAGTGAGTGTATCTTTGAAAAATGGCAGAAAAAGAAATGCCAGATGGGG 1140
Db 1078 CATTCGAGAAGTGAGTGTATCTTTGAAAAAGTGCGCAGAAAAAGAAATAGCAGATGGGT 1137
QY 1141 CCGGTACGTGCTGACCACTCAGAACGACGCGCAGATAAAGTGTCTTCTTCTTCTTCT 1200
Db 1138 CCAGTGCAGTGGCTTGCCACTCAAAAGAAAGGAGCAGACAAAAGTGTCTTCTTCTTCT 1197
QY 1201 AGTGACGCTCCGACCCCTTTGTGACAGTGTGCTGTGGCCACAATGAGGGCAGCGCCAGGAG 1260
Db 1198 AATGAGCTCAACAGTGTGCGATGTACTGTGCGACAGCGGCGAGTCCCACTGAG 1257
QY 1261 AACTCTCAGGATCTGTTCCTCTTGCCTTTAACTTTTGTAGTGAATTCAGAGCCAG 1320
Db 1258 AACTCTCAAGACTCTTCTCCCTTTCCTTTAACTTTTGTGAGTGTACTAAGAGCCAG 1317
QY 1321 AGCATCTGCACAAATACCTGTGTGTCTATCTTGGGGAGCAGACCTCAAGGCGACTAT 1380
Db 1318 ATTATCTGCACAAATACGCTGTGTGTGTCTTCTTTAGAGATTTGATACAAAGACGATTAC 1377
QY 1381 AATGCGCTCAGTGTCTGCCCCCAATATCATCTCATGAAGGAGCCACAGCTTTTCACACA 1440
Db 1378 AATGCTCTCAGTGTCTGCCCCCAAGTACACACTCATGAAGATGCCACTGCTTCTGTGCA 1437
QY 1441 GAACTTCTCAAGCTACGAGAGCATGTTCAGTGAAGAAAAGCTTCAAGCCCTGCCATGAT 1500
Db 1438 GAACTTCTCCATGTCAAGCAGCAGGTGTTCAGCAGGAAAAAGATCATCAAGCCCTGCCAGAT 1497
QY 1501 AGCTGTTACCCCTTTGAG 1518
Db 1498 GGCTGCTGCTCTTGTGAG 1515
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RESULT 13
US-10-175-737-399
; Sequence 399, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-737-399
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Query Match 49.1%; Score 963.6; DB 9; Length 1515;
Best Local Similarity 78.7%; Pred. No. 3e-313;
Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;
```

```
QY 13 CGGGCCATGTTGCTAGTGTGCTGATCTTGGCTGCATCGTCAGAGAGCGCCCTGCTCGA 72
Db 1 CGGGCGATGTCGCTGCTGCTTAAGCCTGCGCGCTGTGCGAGAGCGCGCTATACCCGA 60
QY 73 GAGCGGACTATTTCAGTGTGGCTCTGAGACAGGCGCATCTCCAGAGTGGATGGTCAACAC 132
Db 61 GAGCGGACCGTTCATGTTGGCTCTGAAACTGGGCCAICTCCAGAGTGGATGCTACAAAT 120
QY 133 ACATCACTCCAGGAGACTTGAGGGACCTCCAAGTGGAACTCGTCAAGCAAGTGTGGCA 192
Db 121 GATCTAATCCCGGAGACTTCAGGGACCTCCGAGTAGAACCTGTTACAACCTAGTGTGCA 180
QY 193 GCAGAGGAGTTTCAATTTTGTATGACATAAGCTGGATCTCCGGGCGAGACCCAGCATC 252
Db 181 ACAGGGGACTATTCAATTTTGTATGAATGTAACTGGGTACTCCGGGCGAGATGCCAGCATC 240
QY 253 CGCTTTGTAAGGGCCACCAAGATCTGCGTGAAGTGCAAAAAACAACATGAATTCATACAGC 312
Db 241 CGCTTTGTAAGGGCCACCAAGATTTGTGACGGGCAAAAGCAACTTCAGTCTCTACAGC 300
QY 313 TGTGTGAGGTGCAACTACACAGAGCGCTTCCAAAGCCAGACAGACCTTCCGGCGGCAAA 372
Db 301 TGTGTGAGGTGCAATTACACAGAGCGCTTCCAGACTCAGACAGACCCCTCTGGTGTAAA 360
QY 373 TGGACATTTCTCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCATCAGCGCC 432
Db 361 TGGACATTTCTCTATCATCGGCTTCCCTGTAGAGCTGAAACACAGTCTATTTTATTGGGGCC 420
QY 433 CATACATCTCCCAATGCTAATATGAATGAGCAGACCGCTTCTTTGTCTGTGAATTCACC 492
Db 421 CATATATTTCTTAATGCAAAATATGAATGAGATGGCCCTTTCATGTCTGTGATTTTACC 480
QY 493 TCGCCAGGCTCCCTAAACACAGTAAATGAATATAAAAAAGCAGTGCACCTGAGCGCGGAAGC 552
Db 481 TCACCAGGCTGCCTAGACACACATAATGAATATAAAAAAGTGTGTCAAGSCCGGAAGC 540
QY 553 CTGTGGGAGCCAGACATCACTGCTTTGAAAAAGACGAGAGATGGTTGAAGTGAATTC 612
Db 541 CTGTGGGATCCGAACATCACTGCTTTGTAAGAAAGATGAGGAGACAGTAGAAGTGAATTC 600
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Db 721 GTGACTGGGATAGTGAAGGTGCTACGGTGCAGCTCACTCATAATTTCTACTTGTGGC 780
Qy 784 AATGACTGATCCGACGCGAAGGACAGTGTGCTTGTCTCAGAGCAAGTGTCCCATC 843
Db 781 AGGACTGATCCGACGCGAAGGACAGTGTGCTTGTCCCAAAACAGGCGTCCCTTC 840
Qy 844 CTCCAGATGACAAAGACAGATGCTGGGAGGCTGCTCTCTCTCTCTCTCTCTCTG 900
Db 841 CCTCTGGATAACAAAGACAGCGGAGGCTGCTGCTCTCTCTCTCTCTCTCTCTG 900
Qy 901 CTGGTGGTGTGTGGTGTGTGGGAGTCTACCTAATCTGGAGGCAAGGAGGAC 960
Db 901 CTGGTGGGACATGGTGTGTGGGAGGAGTCTATCTAATGTGGAGGACGAAAGGATC 960
Qy 961 AGAAGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1020
Db 961 AGAAGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1017
Qy 1021 TATCTCTCTGAGATATGTTTCCATCACACCGTCTGCTCTCTCTCTCTCTCTCT 1080
Db 1018 TACCCATCTGAATATGTTTCCATCACACATTTGTTACTTCACTGAATTTCTTCA 1077
Qy 1081 TACTGAGAGTGTGATCTCTCTGAAAAAATGCGAGAAAAAATGCCAGATGGGG 1140
Db 1078 CATTCGAGAAGTCAAGTCTCTCTGAAAAAGTGGCAGAAAAAATAGCAGATGGGT 1137
Qy 1141 CCGGTACGTGCTGACCACTCAGAGCAAGCGGAGATAGTGTCTCTCTCTCTCTCC 1200
Db 1138 CCAAGTCAAGTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1197
Qy 1201 AGTGAGTCTCCGACCTCTGTGACAGTGTCTGTGGCCACAATGAGGCGAGCGCAGG 1260
Db 1198 AATGAGTCTCAACAGTGTGTGCGATGTACTGTGGCAAGCGAGGCGAGTCCAGT 1257
Qy 1261 AACTCTCAGAGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
Db 1258 AACTCTCAAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1317
Qy 1321 ACGCATCTGCACAAATCTCTGCTGTCTATCTGTGGGAGCAGACCTCAAGGCGAC 1380
Db 1318 ATTCACTCTGCACAAATCTCTGCTGTGTCTCTCTCTCTCTCTCTCTCTCTCT 1377
Qy 1381 AATGCGCTCAGTGTCTGCGCCCAATATCTCTCATGAAGGAGCCACAGCTTTCC 1440
Db 1378 AATGCTCTCAGTGTCTGCGCCCAAGTACCACTCTATGAAGGATGCCACTGCT 1437
Qy 1441 GAATCTCTCAAGCTACGAGGAGTGTCTGAGTGAAGAAACGCTCAAGGCTGCG 1500
Db 1438 GAATCTCTCAAGCTACGAGGAGTGTCTGAGTGAAGAAACGCTCAAGGCTGCG 1497
Qy 1501 AGCTGTTTCACTCTGTAG 1518
Db 1498 GGCTGCTGCTCTCTGTAG 1515

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RESULT 15
 US-10-173-706-399
 ; Sequence 399, Application US/10173706
 ; Publication No. US2003022293A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-706-399

Query Match 49.1%; Score 963.6; DB 9; Length 1515;
Best Local Similarity 78.7%; Pred. No. 3e-313;
Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;

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Db 1 CGGGCGATGTGCTGCTGCTGCTAAGCCCTGCGCGCGCTGTGCGAGGAGCGGTATACCCGA 60
Qy 73 GAGCCGACTATTTCAGTGTGGCTCTGAGACAGGCGCATCTCCAGAGTGGTGTCCAAAC 132
Db 61 GAGCCGACCGTTCAATGTGGCTCTGAAACTGGCCATCTCCAGAGTGGTGTCAACAT 120
Qy 133 ACATCTACTCCAGGAGACTTGGAGGACCTCCAAGTGGAACTCGTCAAGCAAGTGTGCA 192
Db 121 GATCTAATCCCGGAGACTTGGAGGACCTCCGAGTAGAACCTGTTACAAC TAGTGTGCA 180
Qy 193 CGAGGAGGATTTTCAATTTTGTATGAACATAAGCTGGATCTCCGGGAGAGCGCAGATC 252
Db 181 ACAGGGGATTTTCAATTTTGTATGAATGTAAAGCTGGGTACTCCGGGCGAGATGCCAG 240
Qy 253 CGTTGTTGAAGGCCACCAAGATCTGCTGAGTGGCAAAAAACAATGAATTCATACAGC 312
Db 241 CGTTGTTGAAGGCCACCAAGATTTGTGAGCGGCAAAAGCACTTCAGTCTCTACAGC 300
Qy 313 TGTGTAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACAGACCTTCCGGCGGCAAA 372
Db 301 TGTGTAGGTGCAATTAACAGAGGCTTCCAGACTCAGACAGACCTCTGGTGTGTA 360
Qy 373 TGGACATTTCTCTATGTAGGCTTCCCTGTGGAGTGAAGTCTCTCTATCTATCAGCGCC 432
Db 361 TGGACATTTCTCTATCAGGCTTCCCTGTAGAGTGAACACAGTCTATTTTCTTGGG 420
Qy 433 CATACATCTCCCAATGTAAATGAATGAGCAGACGCTCTTTGCTGTGTAATTCAC 492
Db 421 CATATATTTCTTAATGCAATATGAATGAAGTGGCTTCCATGTCTGTGAATTCAC 480
Qy 493 TCGCAGGCTGCTAAACCAAGTAAATGAATATAAAAGCAGTGCACGTGAGCGGGAAGC 552
Db 481 TCACCGGCTGCTAGACCAATGAATATAAAAGTGTGTCAAGCGCGGAAGC 540
Qy 553 CTGTGGGACCCAGACATCAGTCTGTGTGTAAGAAAGCAGAGATGGTTGAAGTGAATTC 612
Db 541 CTGTGGGATCCGAAACATCAGTCTGTGTGTAAGAAAGTGAAGAGACAGTAGAAGTGA 600
Qy 613 ACAACCAATCCCTTGGGAAACAGATACAGATTTCTTATTCAACGGGACACGACATTTGG 672
Db 601 ACAACCACTCCCTGGGAAACAGATACAGTCTTTATCCAAACACAGACCTATCATCGG 660
Qy 673 TTTTCTAGAGTGTGG-----AGAAATAACTGATGAGGAGCTGTGTAGCCATCCG 723
Db 661 TTTTCTCAGGTGTTTGAGCCACACAGAAAGAAACAAACGCGAGCTTCAGTGTGATCCA 720
Qy 724 GTGACTGAGGAGTGAAGTGGTGGTTCAGCTGAGCCCATATTTACATACCTGCGGC 783
Db 721 GTGACTGAGGAGTGAAGTGGTTCACGTCGAGCTGACTCCATATTTTCTTACTTGTGG 780
Qy 784 AATGACTCATCTCCGCGAAGGAGCAGTGTGTGCTTTGCTCAGAGCAAGTGTCTCCATC 843
Db 781 AGGACTGCTCCGACATATAAGGAAACAGTGTGTCTGTGCCCAAAACAGGCGTCCCTTC 840
Qy 844 CTCCAGATGACAAAGACGATGCTGGGAGGCTGGCTCTCTCTCTCTCTCTCTCTG 900

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	44.2	2.3	3223	3	US-09-022-255-9
4	44.2	2.3	3223	3	US-08-978-773-3
5	44.2	2.3	3223	3	US-09-022-253-9
6	44.2	2.3	3223	3	US-09-022-260-9
7	44.2	2.3	3223	4	US-09-022-259-9
8	44.2	2.3	3223	4	US-09-022-257-9
9	38	1.9	1364	2	US-08-872-302-3
10	37.4	1.9	1697	4	US-09-346-408-5
11	37.4	1.9	2413	1	US-08-232-463-14
12	37.2	1.9	2416	4	US-09-518-046-1
13	37.2	1.9	2544	4	US-09-518-046-3
14	36.2	1.8	807	4	US-09-715-994-3
15	36.2	1.8	756	2	US-08-530-165-1
16	35.8	1.8	2815	1	US-08-230-491A-1
17	35.8	1.8	2815	2	US-08-619-280A-1
18	35.8	1.8	2815	1	US-08-940-391-1
19	35.2	1.8	6909	2	US-08-804-196-1
20	35.2	1.8	6909	3	US-08-658-340-1
21	35.2	1.8	6909	3	US-08-746-111-26
22	34.6	1.8	2790	3	US-08-718-661-1
23	34.4	1.8	500	3	US-09-141-000-2
24	34.4	1.8	7218	1	US-08-232-463-14
25	34.2	1.7	2311	4	US-09-624-691A-14
26	34.2	1.7	885	3	US-08-651-136C-23
27	34	1.7			

c	28	34	1.7	885	4	US-09-229-911A-23	Sequence 23, Appl
c	29	34	1.7	2073	4	US-09-221-017B-404	Sequence 404, Appl
	30	34	1.7	2226	3	US-08-951-260A-1	Sequence 1, Appl
	31	33.8	1.7	1740	1	US-08-362-512A-3	Sequence 3, Appl
	32	33.8	1.7	1740	4	US-08-964-939-3	Sequence 3, Appl
c	33	33.8	1.7	5697	3	US-08-814-052-11	Sequence 11, Appl
c	34	33.8	1.7	5697	3	US-08-812-829-11	Sequence 11, Appl
	35	33.6	1.7	1264	2	US-08-758-621-13	Sequence 13, Appl
	36	33.6	1.7	1264	4	US-09-107-858-13	Sequence 13, Appl
	37	33.6	1.7	4868	1	US-08-139-937-12	Sequence 12, Appl
	38	33.6	1.7	4868	5	PCT-US93-11310-12	Sequence 12, Appl
	39	33.6	1.7	8789	1	US-08-328-254-5	Sequence 5, Appl
	40	33.6	1.7	10136	1	US-08-353-700-2	Sequence 2, Appl
	41	33.6	1.7	10136	5	PCT-US95-16216-2	Sequence 2, Appl
	42	33.4	1.7	501	4	US-09-326-039-4	Sequence 4, Appl
	43	33.4	1.7	1279	4	US-09-277-716-31	Sequence 31, Appl
	44	33.4	1.7	1279	4	US-09-609-161B-31	Sequence 31, Appl
	45	33.4	1.7	1313	4	US-09-149-476-112	Sequence 112, Appl

ALIGNMENTS

RESULT 1
US-08-620-694A-9
; Sequence 9, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO


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; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: IL-17 R (hCTL8 receptor)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 93..2693
; US-08-620-694A-9

Query Match      2.3%; Score 44.2; DB 2; Length 3223;
Best Local Similarity 45.1%; Pred. No. 0.008;
Matches 224; Conservative 0; Mismatches 258; Indels 15; Gaps 1;

Qy 118 TGAATGTTCAACACACACTCACTCAGGAGACTTGGAGGACCTCAAGTGGAACTCGTC 177
Db 276 TGGATTCACCTCGAACCCTGACCCCTCTCCCAAGGACCTCGAGATCCAGCTGCAC 335
Qy 178 AAGACAAGTGTGGCAGCAGAGAGTTTCAATTTTGTATGAACATAAGCTGGATCTCGG 237
Db 336 TTGCCCCACACCCAAACAGGAGACCTGTTCCCGTGGCTCACATCGAATGGACACTGCAG 395
Qy 238 GCAGAGCCGAGCATCCGCTTGTGAAGCCACCAAGATCTCGGTGAGTGGCAAAACAAAC 297
Db 396 ACAGAGCCGAGCATCCGCTTGTACCTCGAGGTTGACAGTTATCTGT-----C 440
Qy 298 ATGAATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACCAGA 357
Db 441 CTGAGCTGAACACCAATGAACGTTTGTGCGTCAAGTTTGTCTTCTCAAACTGAGG 500
Qy 358 CTTCCCGCGGCAAAATGGACATTTCTCTATAGTGGTTTCCCTGAGGCTGAGCACTCTC 417
Db 501 CATCACCAACAGCGGTGGCGTTTACCTTCAGCCACTTTGTGGTTGACCTGACCCAGGAA 560
Qy 418 TATCTCATCAGGCGCCCAATAACATCCCAATGCTAATGAATGAGGAGCAGCCCTTCTTTG 477
Db 561 TATGAGGTGACCGTTACCACTGCGCAAGCCATCCCTGATGGGACCCAAACCCAG 620
Qy 478 TCTGTGAATCTTCACTCTCGCCAGGCTGCCCTAAACCAACCACTAATGAATAATAAAGCAGTGC 537
Db 621 TCCAAGAAATTTCTTGTGCTGACTGTGAGCAGCCAGGATGAAGTAAACCCAGCTGC 680
Qy 538 ACTGAGCGGGAAGCCTGTGGGACCCAGACATCACTGCTTGTATAAAGAACAGAGATG 597
Db 681 ATGAGCTCAGGAGCCTGTGGGACCCCAACATCACTCCGCGGAGACCTCGGAGCCACCAG 740
Qy 598 GTTGAAGTGAATTTTAC 614
Db 741 CTGCGTGTGAGCTTAC 757

RESULT 2
US-09-022-255-9
; Sequence 9, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
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RESULT 3
US-09-022-696--9
; Sequence 9, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: IL-17 R (hCTLA8 receptor)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 93..2693
US-09-022-696--9

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	Query Match	2.3%;	Score 44.2;	DB 3;	Length 3223;
	Best Local Similarity	45.1%;	Pred. No. 0.008;		
	Matches 224;	Conservative 0;	Mismatches 258;	Indels 15;	Gaps 1;
Qy	118	TGGATGGTCCAAACACACACTCACTCCAGGAGACTTGAGGGACCTCCAAGTGGAACTCGTC	177		
Db	276	TGGAATCACCTCGAAACCTGACCCCTCTCCCCAAAGGACCTCGAGTCAGCTGCAC	335		
Qy	178	AAGACAAGTGGTGAGCAGAGAGGATTTTCAATTTTGATGAACATAAGCTGGATATCTCCGG	237		
Db	336	TTTGCCACACCCAAAGGAGACCTGTTCCCGTGGCTCATCGAATGGACATCGAG	395		
Qy	238	GCAGACGCGCAGCATCCGCTTGTGAAGGCCACCAAGATCTGGTGAGTGGCAAAAACAC	297		

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QY 298 ATGAATTCATACAGCTGTGTGAGGTGCACACTACACAGAGCGCTTCCAAAGCCACGACCAGA 357
DB 441 CTGCAGCTGAACACCAATGAACGTTTGTGCGCTCAGGTTTGAGTTTCTGTCCAAACTGAGG 500
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DB 501 CATCACACAGCGCGTGGCGTTTACCTTTACGACCATTTTGTGGTTGACCCCTGACCCAGGAA 560
QY 418 TATCTCATCAGCGCCCATACATACCTCCCAATGCTAATATGAATCAGGACAGCCCTTCTTTG 477
DB 561 TATGAGGTGACCGTTTACCACCTTGCCCAAGCCCATCCCTGATGGGACCCCAAAACCACAG 620
QY 478 TCTGTGAACTTCACCTCGCCAGCGCTGCCTAAACACAGGTAATGAAATATATAAAAGCAGTGC 537
DB 621 TCCAAGAAATTCCTGTGTCCTGACTGTGAGCACGCCAGGATGAAGTTAACCCGCCATGC 680
QY 538 ACTGAGCGGGAGCGCTGTGGGACCCAGACATCATCTGCTTGTAAAAAGAACGAGAAGATG 597
DB 681 ATGAGCTCAGGCGCTGTGGGACCCCAACATCACCGTGGAGACCCCTGGAGGCCACCAG 740
QY 598 GTTCAAGTGAATTCAC 614
DB 741 CTGCGTGTGAGCTTCAC 757

RESULT 4
US-08-978-773-3
; Sequence 3, Application US/08978773
; Patent No. 6083906
; GENERAL INFORMATION:
; APPLICANT: Troutt, Anthony
; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple PowerMacintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,773
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 60/052,525
; FILING DATE: 27 NOVEMBER 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2623-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:

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ORGANISM: Human
IMMEDIATE SOURCE:
CLONE: IL-17R
FEATURE:
NAME/KEY: CDS
LOCATION: 93...2690
US-08-978-773-3

Query Match 2.3%; Score 44.2; DB 3; Length 3223;
Best Local Similarity 45.1%; Pred. No. 0.008;
Matches 224; Conservative 0; Mismatches 258; Indels 15; Gaps 1;
QY 118 TGGATGTCACACACACACTCACTCCAGGAGACTTGGAGGACCTCCAAAGTGAACCTCGTC 177
DB 276 TGGATTCACCTCGAAACCTGACCCCTCTCTCCCAAGGACCTGAGATCCAGCTGCAC 335
QY 178 AAGACAAGTGTGGCAGAGAGAGTTTCAATTTGATGAACAATAAGCTGGATACCTCCGG 237
DB 336 TTTGCCCCACACCCCAAGAGAGACCTGTTCCCGTGGCTCACATCGAATGGACACTGCAG 395
QY 238 GCAGAGCCAGCATCCGCTGTTGTAAGGCCACCAAGATCTGCTGAGTGGCAAAACACAC 297
DB 396 ACAGAGCCAGCATCTGTACCTCGAGGGTGCAGAGTTATCTGT-----C 440
QY 298 ATGAATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACAGA 357
DB 441 CTGCAGCTGAACCAACCAATGAACGTTTGTGCGTCAGGTTTGAGTTTCTGTCCAACTGAG 500
QY 358 CTTCCGGCGGCAAAATGGACAATCTCTATGTAGGCTTCCCTGTGAGCTGAGCACTCTC 417
DB 501 CATCACACAGCGGTGGCGTTTACCTTTAGCCCACTTTGTGCTTACCTGACCCAGGAA 560
QY 418 TATCTCATCAGCGCCCATACATCCCAATGCTAATATGAATGAGGACAGCCCTTCTTTG 477
DB 561 TATGAGGTGACCGTTTCCACCCTGCCCCAAGCCCATCCCTGATGGGACCCCAACACACAG 620
QY 478 TCTGTGAATTCACCTCGCCAGGCTGCTTAAACCAAGCTGTAATGAATATAAAGAGAGTGC 537
DB 621 TCCAAAGAAATTTCTTGTGCTGCTGACTGTGAGCAGCCAGGATGAAGGTAACCCAGCTGC 680
QY 538 ACTGAGCGGGAAGCCTGTGGAGCCAGACATCACTGCTTTGTAAGAAACAGAGAGATG 597
DB 681 ATGAGCTCAGGCAGCGCTGTGGAGCCCAACATCACCGTGGAGACCCCTGGAGGCCACCA 740
QY 598 GTTGAAGTGAATTTTAC 614
DB 741 CTGCGTGTGAGCTTAC 757

RESULT 5

US-09-022-253-9
Sequence 9, Application US/09022253
Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022.253

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
FEATURE:
NAME/KEY: CDS
LOCATION: 93...2693
US-09-022-253-9

Query Match 2.3%; Score 44.2; DB 3; Length 3223;
Best Local Similarity 45.1%; Pred. No. 0.008;
Matches 224; Conservative 0; Mismatches 258; Indels 15; Gaps 1;
QY 118 TGGATGTCACACACACTCACTCCAGGAGACTTGGAGGACCTCCAAAGTGAACCTCGTC 177
DB 276 TGGATTCACCTCGAAACCTGACCCCTCTCTCCCAAGGACCTGAGATCCAGCTGCAC 335
QY 178 AAGACAAGTGTGGCAGAGAGAGTTTCAATTTGATGAACAATAAGCTGGATACCTCCGG 237
DB 336 TTTGCCCCACACCCCAAGAGAGACCTGTTCCCGTGGCTCACATCGAATGGACACTGCAG 395
QY 238 GCAGAGCCAGCATCCGCTTGTGAAAGGCCACCAAGATCTCGTGGTGGCAAAACACAC 297
DB 396 ACAGAGCCAGCATCTGTACCTCGAGGGTGCAGAGTTATCTGT-----C 440
QY 298 ATGAATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACAGA 357
DB 441 CTGCAGCTGAACCAACCAATGAACGTTTGTGCGTCAGGTTTGTGCTTCTGTCCAACTGAG 500
QY 358 CTTCCGGCGGCAAAATGGACAATCTCTATGTAGGCTTCCCTGTGAGCTGAGCACTCTC 417
DB 501 CATCACACAGCGGTGGCGTTTACCTTTAGCCCACTTTGTGCTTACCTGACCCAGGAA 560
QY 418 TATCTCATCAGCGCCCATACATCCCAATGCTAATATGAATGAGGACAGCCCTTCTTTG 477
DB 561 TATGAGGTGACCGTTTCCACCCTGCCCCAAGCCCATCCCTGATGGGACCCCAACACACAG 620
QY 478 TCTGTGAATTCACCTCGCCAGGCTGCTTAAACCAAGCTGTAATGAATATAAAGAGAGTGC 537
DB 621 TCCAAAGAAATTTCTTGTGCTGCTGACTGTGAGCAGCCAGGATGAAGGTAACCCAGCTGC 680
QY 538 ACTGAGCGGGAAGCCTGTGGAGCCAGACATCACTGCTTTGTAAGAAACAGAGAGATG 597
DB 681 ATGAGCTCAGGCAGCGCTGTGGAGCCCAACATCACCGTGGAGACCCCTGGAGGCCACCA 740
QY 598 GTTGAAGTGAATTTTAC 614

Db 741 CTGCGTGTGAGCTTCAC 757
|||||
RESULT 6
US-09-022-260-9
; Sequence 9, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION NUMBER: US/09/022,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: IL-17 R (hCTL8 receptor)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 93..2693
US-09-022-260-9
Query Match 2.3%; Score 44.2; DB 3; Length 3223;
Best Local Similarity 45.1%; Pred. No. 0.008;
Matches 224; Conservative 0; Mismatches 258; Indels 15; Gaps 1;
Qy 118 TGGATGGTCCACACACTCTACTCCAGGAGCTTGAGGAGCTTCAAGTGGAACTCGTC 177
|||||
Db 276 TGGATTACCTCGAAACCTGACCTCCCTCCCAAGAGAGCTGCAGATCCAGCTGCAC 335
Qy 178 AAGACAAGTGTGGCAGCAGAGAGTTTCAATTTTGAATGAATAGCTGGATCTCCGG 237
Db 336 TTGCGCCACCCACACAGAGAGACTGTTCCCGCGGCTCAGATCGAATGGACACTGCAG 395

Qy 238 GCAGAGCCGAGCATCCGCTTGTGTGAAGGCCACCAAGATCTGCGTGAAGTGGCAAAACAAC 297
|||||
Db 396 ACAGAGCCGAGCATCTGTACCTCGAGGGTGCAGAGTTATCTGT-----C 440
Qy 298 ATGAATTCATACAGCTGTGTGAGGTGCACTACACAGAGSCCTTCCAAAGCCAGACAGA 357
|||||
Db 441 CTGAGCTGAACACCAATGAAGTTTGTGCGTCAAGTTTGTGAGTTTCTGCCAAACTGAGG 500
Qy 358 CCTTCGGCGGCAAAATGGACATTTCTCTATGTAGGCTTCCCTGTGAGCTGAGCACTCTC 417
|||||
Db 501 CATCACCACAGCGGTGGGTTTACCTTCAGCCACTTTGTGCTTGCCTGCACAGGAA 560
Qy 418 TATCTCATCAGCGGCCCATTAACATCCCAATGCTAATATGAATGAGGACAGCCCTTCTTTG 477
|||||
Db 561 TATGAGGTGACCGTTTCAACACCTGCCCCAAGCCCATCCCTGATGGGAGCCCAACCAAC 620
Qy 478 TCTGTGAACCTTCACCTCGCCAGCGCTGCTTAAACACAGTAATGAATATATAAAGCAGTGC 537
|||||
Db 621 TCAGAATTTCTTGTGCTCTGACTGTGAGCAGCCGAGGATGAAGTAAACCGCCATGC 680
Qy 538 ACTGAGCGGGGAAGCCTGTGGGACCCAGACATCACTGCTTGTAAAAAGAACGAGAAGATG 597
Db 681 ATGAGCTCAGGAGCGCTGTGGGACCCCAACATCACCGTGGAGACCCCTGGAGGCCAC 740
Qy 598 GTTGAAGTGAATTTTCAC 614
Db 741 CTGCGTGTGAGCTTCAC 757
RESULT 7
US-09-022-259-9
; Sequence 9, Application US/09022259
; Patent No. 6191104
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:

LENGTH: 3223 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN: IL-17 R (hCTL8 receptor)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 93..2693
 US-09-022-259-9

Query Match 2.3%; Score 44.2; DB 4; Length 3223;
 Best Local Similarity 45.1%; Pred. No. 0.008;
 Matches 224; Conservative 0; Mismatches 258; Indels 15; Gaps 1;

QY 118 TGGATGGTCCAAACACACACTCACTCCAGGAGACTTGGAGGACCTCCAAAGTGAACCTCGTC 177
 Db 276 TGGATTCACCTCGAACCCTGACCCCTCTCCCAAGGACCTGCAGATCCAGCTGCAC 335
 QY 178 AGACAAGTGTGGCAGCAGAGGAGTTTCAATTTTGAATGAACATAAGCTGGATATCCGG 237
 Db 336 TTTGCCACACACCCCAACAGGAGACCTGTTCCCGTGGCTCACATCGAATGGACACTGCAG 395
 QY 238 GCAGCGCCAGCATCCGCTGTTGAAGGCCACCAAGACTCGGTGAGTGGCAAAACACAC 297
 Db 396 ACAGCGCCAGCATCTGTACCTCGAGGGTGCAGATTTATCTGT-----C 440
 QY 298 ATGAATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACACAG 357
 Db 441 CTGCAGCTGAACACCAATGAACGTTTGTGGTCAGGTTTGTGTTCTGTCCAACTGAGG 500
 QY 358 CCTTCGGGGGGAATGGACATCTCTATGTAGGTTCCCTGTGGAGCTGAGCACTCTC 417
 Db 501 CATCACCAGCGGTGGGGTTTACCTTCAGCCACTTGTGGTGGAGTGAAGTGAACGCAATGC 680
 QY 538 ACTGAGCGGGAGCCTGTGGGACCCAGACATCACTGCTTTGTAAGAAAGAACAGAGATG 597
 Db 681 ATGAGCTCAGGAGCCTGTGGGACCCCAACATCACCCTGGAGACCTGGAGGCCACCAG 740
 QY 598 GTTGAAGTGAATTTTAC 614
 Db 741 CTGCGTGTGAGCTTAC 757

RESULT 8
 US-09-022-257-9
 Sequence 9, Application US/09022257
 Patent No. 6197525
 GENERAL INFORMATION:
 APPLICANT: Yao, Zhengbin
 APPLICANT: Spriggs, Melanie
 APPLICANT: Fanslow, William
 TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/022.257
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/620,694
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/410,535
 FILING DATE: 23 MARCH 1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,695
 REFERENCE/DOCKET NUMBER: 2617-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3223 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN: IL-17 R (hCTL8 receptor)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 93..2693
 US-09-022-257-9

Query Match 2.3%; Score 44.2; DB 4; Length 3223;
 Best Local Similarity 45.1%; Pred. No. 0.008;
 Matches 224; Conservative 0; Mismatches 258; Indels 15; Gaps 1;

QY 118 TGGATGGTCCAAACACACACTCACTCCAGGAGACTTGGAGGACCTCCAAAGTGAACCTCGTC 177
 Db 276 TGGATTCACCTCGAACCCTGACCCCTCTCCCAAGGACCTGCAGATCCAGCTGCAC 335
 QY 178 AAGACAAGTGTGGCAGCAGAGGAGTTTCAATTTTGAATGAACATAAGCTGGATATCCGG 237
 Db 336 TTTGCCACACCCCAACAGGAGACCTGTTCCCGTGGCTCACATCGAATGGACACTGCAG 395
 QY 238 GCAGCGCCAGCATCCGCTGTTGAAGGCCACCAAGACTCGGTGAGTGGCAAAACACAC 297
 Db 396 ACAGCGCCAGCATCTGTACCTCGAGGGTGCAGATTTATCTGT-----C 440
 QY 298 ATGAATTCATACAGCTGTGTGAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACACAG 357
 Db 441 CTGCAGCTGAACACCAATGAACGTTTGTGGTGGAGTGAAGTGAACGCAATGCAGG 500
 QY 358 CCTTCGGGGGGAATGGACATCTCTATGTAGGTTCCCTGTGGAGCTGAGCACTCTC 417
 Db 501 CATCACCAGCGGTGGGGTTTACCTTCAGCCACTTGTGGTGGAGTGAAGTGAACGCAATGC 560
 QY 418 TATCTCATCAGCGGCCCAATACATCCCAATGCTAATGAATGAAGAGCAGCCCTTCTTTG 477
 Db 561 TATGAGGTGACCGTTTCACTACCACTGCCCAAGCCATCCCTGATGGGGACCCCAACACAC 620
 QY 478 TCTGTGAACCTTCACTCGCCAGGCTGCTAAACCCAGCTAATGAATATAAAAGCAGTG 537
 Db 621 TCCAGAAATTTCTTGTGCTGACTGTGAGCAGCCAGGATGAAGTAAACCCGATGC 680

QY 538 ACTGAGCGGGAAGCCTGTGGGACCCAGACATCACTGCTTGTAAAGAACGAGAGATG 597
Db 681 ATGAGCTCAGGAGCCTGTGGGACCCCAACATCACCGTGGAGACCTGGAGGCCACCCAG 740
QY 598 GTTGAAGTGAATTTCAC 614
Db 741 CTGCGTGTGAGCTTCAC 757

RESULT 9
US-08-872-302-3
; Sequence 3, Application US/08872302
; Patent No. 5846784
; GENERAL INFORMATION:
; APPLICANT: Hitz, William D
; TITLE OF INVENTION: Fatty Acid Modifying Enzymes From
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. duPont de Nemours and Co.
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,302
; FILING DATE:

CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R
; REGISTRATION NUMBER: P-41,173
; REFERENCE/DOCKET NUMBER: BB-1084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1364 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1254

US-08-872-302-3

Query Match 1.9%; Score 38; DB 2; Length 1364;
Best Local Similarity 71.4%; Pred. No. 0.33;
Matches 50; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1894 TTTTGTAACTTTTAACTGTTAATCAATAATCCGTTTGGGAGCTCTCAAAAAAAAAA 1953
Db 1288 TTTTGTAACTTTTGTAACTAATAATAATAATCTTGAATGAGATAAAAAAAAAA 1347

QY 1954 AAAAAAAAAA 1963
Db 1348 AAAAAAAAAA 1357

RESULT 10
US-09-346-408-5
; Sequence 5, Application US/09346408B
; Patent No. 6338966
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Anderson, Shawn

; APPLICANT: Falco, Carl
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
; FILE REFERENCE: BB-1167-A
; CURRENT APPLICATION NUMBER: US/09/346,408B
; CURRENT FILING DATE: 1999-07-01
; EARLIER APPLICATION NUMBER: 60/092,833
; EARLIER FILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 1697
; TYPE: DNA
; ORGANISM: Glycine max
US-09-346-408-5

Query Match 1.9%; Score 37.4; DB 4; Length 1697;
Best Local Similarity 64.4%; Pred. No. 0.56;
Matches 56; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1877 ATGCTGCAGTAGACCGTTTGTAACTTTTAACTGTTAATCAATAATCCGTTTGGGAA 1936
Db 1609 ATACTTCAGGAGGATCCTCTGSCCAATCTAATAATAATAATAATAATAATAATAA 1668
QY 1937 GCTCTCAAAAAAAAAAAAAAAAAAAAAA 1963
Db 1669 GGCAAAAAAAAAAAAAAAAAAAAAA 1695

RESULT 11
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149

INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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;
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZgpt-F1s
US-08-232-463-14

Query Match 1.9%; Score 37.4; DB 1; Length 7218;
Best Local Similarity 3.6%; Pred. No. 1.2;
Matches 14; Conservative 209; Mismatches 170; Indels 0; Gaps 0;

Qy 511 CAGCTAATGAATATAAAAGACAGTGCAGTGGCGGAGCTGTGGACCGACGACATC 570
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1435 CRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1376

Qy 571 ACTGCTTTAAAGAACGACGAGATGGTTGAAGTAAATTTCAACACCAATCCCTTGA 630
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1375 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1316

Qy 631 AACAGATACAGATTCATTCACCGGACGACGATCGGGTTTCTAGAGTGTGGAG 690
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1315 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1256

Qy 691 AATAAACTGATGAGGAGCTGTGAGCCATCCCGGTGACTGAGGAGTCAAGTGCGGTG 750
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1255 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1196

Qy 751 GTTCACTGACCCCAATATTACATACCTCGGCAATGACTGCATCCGACGCGGACGA 810
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1195 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1136

Qy 811 GTTGCTCTTCTCAGACAGAGTGTCCATCCCTCCAGATGACACAGACGATGCTG 870
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1135 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1076

Qy 871 GGAGGCTGCTGCTCTCTCTCTCTGCTGCTGCTG 903
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1075 RRRRRRRRATCGAAGCTCCCTCGACCTGCAG 1043

RESULT 12
US-09-518-046-1
; Sequence 1, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 1
; LENGTH: 2413
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 gene
US-09-518-046-1

Query Match 1.9%; Score 37.2; DB 4; Length 2413;
Best Local Similarity 63.3%; Pred. No. 0.77;
Matches 57; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1874 TCTATGCTGACGAGTACCGTTTGTAACTTTTAACTGTTAATGAATATCCGTTTGG 1933
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2313 TCTTTGTAGCATTTGGTGTGCTTGAAGTATTATTGCTTTGATTCCAAATAATATGTTCC 2372

Qy 1934 GAAGCTCTCAAAAAAAAAAAAAAAAAAAAAA 1963
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2373 TTCCCTCAAAAAAAAAAAAAAAAAAAAAA 2402

RESULT 13
US-09-261-416-1
; Sequence 1, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261.416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 1
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 144..1511
; OTHER INFORMATION: CDS
US-09-261-416-1

Query Match 1.9%; Score 37.2; DB 4; Length 2416;
Best Local Similarity 63.3%; Pred. No. 0.77;
Matches 57; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1874 TCTATGCTGACGAGTACCGTTTGTAACTTTTAACTGTTAATGAATATCCGTTTGG 1933
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2316 TCTTTGTAGCATTTGGTGTGCTTGAAGTATTATTGCTTTGATTCCAAATAATATGTTCC 2375

Qy 1934 GAAGCTCTCAAAAAAAAAAAAAAAAAAAAAA 1963
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2376 TTCCCTCAAAAAAAAAAAAAAAAAAAAAA 2405

RESULT 14
US-09-518-046-3
; Sequence 3, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 3
; LENGTH: 2544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 variant gene
US-09-518-046-3

Query Match 1.9%; Score 37.2; DB 4; Length 2544;
Best Local Similarity 63.3%; Pred. No. 0.79;
Matches 57; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1874 TCTATGCTGACGAGTACCGTTTGTAACTTTTAACTGTTAATGAATATCCGTTTGG 1933
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2444 TCTTTGTAGCATTTGGTGTGCTTGAAGTATTATTGCTTTGATTCCAAATAATATGTTCC 2503

Qy 1934 GAAGCTCTCAAAAAAAAAAAAAAAAAAAAAA 1963
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2504 TTCCCTCAAAAAAAAAAAAAAAAAAAAAA 2533
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Search completed: May 28, 2003, 10:22:39
Job time : 118.256 secs

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XX 04-FEB-2000; 2000US-0180374.
PR (UYAR-) UNIV ARKANSAS.
PA Shaughnessy JD;
PI MPI; 2001-496920/54.
DR P-PSDB; AAE07162.
XX
XX New nucleic acids encoding an interleukin (IL)-17 receptor related
PT protein for use as a marker for leukemia
XX
XX Claim 1a; Page 76-77; 87bp; English.
XX
CC The present sequence is a cDNA encoding mouse interleukin (IL)-17
CC receptor related protein (Evi27). Mouse Evi27 gene was mapped to
CC chromosome 14. Evi27 is a common site of retroviral integration
CC in BKH murine myeloid leukaemias. Evi27 cDNA sequences are useful
CC as antisense molecules to inhibit Evi27 protein or for chromosomal
CC mapping or mutational analysis of Evi27 protein. They are proviral
CC integration sites associated with leukemias and monitoring this
CC site provides a genetic tag for disease gene identification. The
CC proteins of the invention are useful to stimulate the secretion of
CC proinflammatory cytokines such as IL-8 and plays an important role
CC in the developmental and/or disease processes of haematopoietic
CC cells. Hence modulating the expression of Evi27 at the RNA or
CC protein level is used in the treatment of diseases such as cancer
CC or autoimmune diseases.
XX
XX Sequence 1963 BP; 510 A; 492 C; 494 G; 467 T; 0 other;
SQ
Query Match 100.0%; Score 1963; DB 22; Length 1963;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1963; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGGCCAGTGGCCGCGCCATGTTCTAGTGTCTGATCTTGGCTGCATCGTGCAGAGC 60
Db 1 GTGGCCAGTGGCCGCGCCATGTTCTAGTGTCTGATCTTGGCTGCATCGTGCAGAGC 60
QY 61 GCCCTGCTGAGAGCGGAGCTATTCACTGCTCTGAGACAGGCGCATCTCCAGAGTGG 120
Db 61 GCCCTGCTGAGAGCGGAGCTATTCACTGCTCTGAGACAGGCGCATCTCCAGAGTGG 120
QY 121 ATGTGCAACACACACTCACTCCAGAGAGCTTGAGGAGCCTCCAAAGTGAATCGTCAAG 180
Db 121 ATGTGCAACACACACTCACTCCAGAGAGCTTGAGGAGCCTCCAAAGTGAATCGTCAAG 180
QY 181 ACAAGTGTGACAGAGAGATTTCATTTTGAATGAACAATAAGCTGATATCTCCGGCA 240
Db 181 ACAAGTGTGACAGAGAGATTTCATTTTGAATGAACAATAAGCTGATATCTCCGGCA 240
QY 241 GAGCGCAGATCCGCTTGTGAAGGCCACCAAGATCTGCTGATGCAAAAACAATG 300
Db 241 GAGCGCAGATCCGCTTGTGAAGGCCACCAAGATCTGCTGATGCAAAAACAATG 300
QY 301 AATTTCATAGAGCTGTGTGAGGTGCACTACAGAGGCTTCCAAAGCCAGACCAAGCT 360
Db 301 AATTTCATAGAGCTGTGTGAGGTGCACTACAGAGGCTTCCAAAGCCAGACCAAGCT 360
QY 361 TCCGGCGGCAATGAGATCTTCTATGTAGGCTTCCCTGTGAGAGCTGACACTCTAT 420
Db 361 TCCGGCGGCAATGAGATCTTCTATGTAGGCTTCCCTGTGAGAGCTGACACTCTAT 420
QY 421 CTATCAGCGCCCAATACATCCCAATGCTAATATGAAATGAGGACGCTTCTTTGTCT 480
Db 421 CTATCAGCGCCCAATACATCCCAATGCTAATATGAAATGAGGACGCTTCTTTGTCT 480
QY 481 GTGAACCTCACTCGCCAGGCTGCTTAAACAGTAAATGAATTAATAAGAGCTGACT 540
Db 481 GTGAACCTCACTCGCCAGGCTGCTTAAACAGTAAATGAATTAATAAGAGCTGACT 540
QY 541 GAGCGGGAAGCTGTGTGAGACCAAGATCATCTGCTTGAAGAAAGAGAGATGCTT 600

Db 541 GAGCGGGAAGCTGTGTGAGACCAAGATCATCTGCTTGAAGAAAGAGAGATGCTT 600
QY 601 GAAGTAATTTTCAACCAATCCCTTTGAAACAGATAAGATTTCTATTCAACGGGAC 660
Db 601 GAAGTAATTTTCAACCAATCCCTTTGAAACAGATAAGATTTCTATTCAACGGGAC 660
QY 661 ACAGCATTTGGGGTTTCTAGAGTGTGAGAAATTAATGATGAGAGAGCTGTAGCATC 720
Db 661 ACAGCATTTGGGGTTTCTAGAGTGTGAGAAATTAATGATGAGAGAGCTGTAGCATC 720
QY 721 CCGGTACTGAGAGAGTGAAGTGGGTGCTTACCTGACCTGACCCATATTTACATCTGC 780
Db 721 CCGGTACTGAGAGAGTGAAGTGGGTGCTTACCTGACCTGACCCATATTTACATCTGC 780
QY 781 GGAATGACTGCACTCCGAGCGCAAGGAGAGATTTGCTTGCAGAGCAAGTGTCTCC 840
Db 781 GGAATGACTGCACTCCGAGCGCAAGGAGAGATTTGCTTGCAGAGCAAGTGTCTCC 840
QY 841 ATCCCTTCAGATGACACAGACGATGCTGGAGGCTGCTCTCTCTCTGAGTGTG 900
Db 841 ATCCCTTCAGATGACACAGACGATGCTGGAGGCTGCTCTCTCTCTGAGTGTG 900
QY 901 CTGTGGCTGTGTGGGTGTGCTGAGCTGGGATCTTACCTTAACCTTGAAGGCAAGAGAC 960
Db 901 CTGTGGCTGTGTGGGTGTGCTGAGCTGGGATCTTACCTTAACCTTGAAGGCAAGAGAC 960
QY 961 ACAGAAAGCTCTTTCTTATTTTCCACATGCTCTGCTCCCTATTAAGTCTGTGTGTT 1020
Db 961 ACAGAAAGCTCTTTCTTATTTTCCACATGCTCTGCTCCCTATTAAGTCTGTGTGTT 1020
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Db 1021 TATCTTCTGAGATATGTTTCCATCAGACGCTGTGCTTCACTGACTTCTTCAAAAC 1080
QY 1081 TACTGAGAAAGTGAAGTCACTTGAATAATGAGCAAAATGCGCAGATGGGG 1140
Db 1081 TACTGAGAAAGTGAAGTCACTTGAATAATGAGCAAAATGCGCAGATGGGG 1140
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Db 1141 CCGGTACAGTGTGCTGACCACTGAGAAAGGAGGAGATTAAGTGTCTTCTTCTCC 1200
QY 1201 AGTACGTCCTCCAGCCTTTGTGACAGTGTGCTGACCAATGAGAGGCGCCAGAGAG 1260
Db 1201 AGTACGTCCTCCAGCCTTTGTGACAGTGTGCTGACCAATGAGAGGCGCCAGAGAG 1260
QY 1261 AACTCTCAGAGATCTGTTCCCTCTTGAACCTTTTGTAGTATTCAGAGCAG 1320
Db 1261 AACTCTCAGAGATCTGTTCCCTCTTGAACCTTTTGTAGTATTCAGAGCAG 1320
QY 1321 AGGATCTGCAAAATACCTGCTGTCTTCTTGGGGAGAGAGACCTCAAGGCCACTAT 1380
Db 1321 AGGATCTGCAAAATACCTGCTGTCTTCTTGGGGAGAGAGACCTCAAGGCCACTAT 1380
QY 1381 AATGCTCAGTGTGTGCGCCCAATATATCTCATGAAGAGAGGCCAGCTTCCACACA 1440
Db 1381 AATGCTCAGTGTGTGCGCCCAATATATCTCATGAAGAGAGGCCAGCTTCCACACA 1440
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Db 1441 GAACTTCTCAAGGCTTACAGAGAGATGTCAAGTGAAGAAACGCTCAAGCCTGATAT 1500
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Db 1501 AGCTGTTCACTCTTGTAGTCCACCGGGGGAATTAAGACTGTGAAGCTTCTATCTTC 1560
QY 1561 CTTCAGTGAAGAAATGCTGTGAGAGCTGAAATGTGTGGAGAGAGCTGTGTGAGGT 1620
Db 1561 CTTCAGTGAAGAAATGCTGTGAGAGCTGAAATGTGTGGAGAGAGCTGTGTGAGGT 1620
QY 1621 AGTGTATGTACAACTGCTTTAAATGAGTGTGCAAAAGTCAACCTGACATACAG 1680

Db 1621 AGTCTATGTACAACTGCTTTAAAACTGAGTTTGCAAGTCAACCTGAGCATACAG 1680
 QY 1681 CCTGAGGAGTACATGCTGATTTATGAGCAACACAGATTACAGATATGAGTG 1740
 Db 1681 CCTGAGGAGTACATGCTGATTTATGAGCAACACAGATTACAGATATGAGTG 1740
 QY 1741 GGAACCTACATTTGGGATATACCAAAAGCTGGGTAATGATTTATCATCTAGAACACGACCT 1800
 Db 1741 GGAACCTACATTTGGGATATACCAAAAGCTGGGTAATGATTTATCATCTAGAACACGACCT 1800
 QY 1801 CTGGGCAATGAATATACGCACTTCCCTGCTGAGGCTGCTGCAAGTGGGCTGCTT 1860
 Db 1801 CTGGGCAATGAATATACGCACTTCCCTGCTGAGGCTGCTGCAAGTGGGCTGCTT 1860
 QY 1861 GCACTGCAATGCTCTATGCTGCAAGTACGCTTTTGAACATTTATCTGTTATGA 1920
 Db 1861 GCACTGCAATGCTCTATGCTGCAAGTACGCTTTTGAACATTTATCTGTTATGA 1920
 QY 1921 ATTAATCCGTTGGGAAAGCTCTCAAAAAA 1963
 Db 1921 ATTAATCCGTTGGGAAAGCTCTCAAAAAA 1963

RESULT 2

AAD13446 ID AAD13446 standard; cDNA; 2589 BP.
 AC AAD13446;

XX 06-NOV-2001 (first entry)
 DT Mouse interleukin-17 receptor related protein (Evi127) encoding cDNA #2.

DE Mouse interleukin-17 receptor related protein (Evi127) encoding cDNA #2.

XX Mouse; interleukin-17 receptor related protein; IL-17; chromosome 14;
 KW Evi127; retroviral integration; chromosomal mapping; mutational analysis;
 KW BXH2 murine myeloid leukaemia; proinflammatory cytokine; IL-8; therapy;
 KW haematopoietic cell; cancer; autoimmune disease; B8.

OS Mus sp.

XX Location/Qualifiers
 PH Key 19..1511
 FT CDS /*tag= d

FT /*product= "Mouse Evi127 protein"
 FT /transl_except= "(pos:162..163, aa:Cys-Leu)"
 FT /note= "Insertion of 626 bases alters the reading
 FT frame; CDS does not include stop codon"
 FT /partial

XX W0200157202-A2.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US03518.

XX 04-FEB-2000; 2000US-0180374.

XX (UYAR-) UNIV ARKANSAS.

XX Shaughnessy JD;

XX WPI; 2001-496920/54.

XX P-PSDB; AAB07163.

XX New nucleic acid encoding an interleukin (IL)-17 receptor related
 XX protein for use as a marker for leukemia

XX Claim 1a; Page 77-78; 87bp; English.

CC The present sequence is a cDNA encoding mouse interleukin (IL)-17
 CC receptor related protein (Evi127). Mouse Evi127 gene was mapped to
 CC chromosome 14. Evi127 is a common site of retroviral integration
 CC in BXH2 murine myeloid leukaemias. Evi127 cDNA sequences are useful

CC as antisense molecules to inhibit Evi127 protein or for chromosomal
 CC mapping or mutational analysis of Evi127 protein. They are proviral
 CC integration sites associated with leukemias and monitoring this
 CC site provides a genetic tag for disease gene identification. The
 CC proteins of the invention are useful to stimulate the secretion of
 CC proinflammatory cytokines such as IL-8 and plays an important role
 CC in the developmental and/or disease processes of haematopoietic
 CC cells. Hence modulating the expression of Evi127 at the RNA or
 CC protein level is used in the treatment of diseases such as cancer
 CC or autoimmune diseases.

XX Sequence 2589 BP; 642 A; 628 C; 643 G; 676 T; 0 other;

Query Match 75.0%; Score 1472.2; DB 22; Length 2589;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1474; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 487 TTCACCTGCGCAGGCTGCTTAAACCAAGTAATATATAAAGACGCTGAGGCG 546

Db 1113 TTCACATTCGCCAGGCTGCTTAAACCAAGTAATATATAAAGACGCTGAGGCG 1172

QY 547 GGAAGCTGTGGGAGCCAGACATCACTGCTTAAAGAAAGAGAGATGTTGAAGTG 606

Db 1173 GGAAGCTGTGGGAGCCAGACATCACTGCTTAAAGAAAGAGAGATGTTGAAGTG 1232

QY 607 AATTTCACACCAATCCCTTGAAGAGATACAGATTCTCATTCACGGGACAGACA 666

Db 1233 AATTTCACACCAATCCCTTGAAGAGATACAGATTCTCATTCACGGGACAGACA 1292

QY 667 TTGGGGTTTTCTAGAGTGTGGAGATTAATAGATGAGGACGTCTGTAGCCATCCCGGTG 726

Db 1293 TTGGGGTTTTCTAGAGTGTGGAGATTAATAGATGAGGACGTCTGTAGCCATCCCGGTG 1352

QY 727 ACTGAGGAGAGAGAGTGGTGGTTCAGCTGACGCCATATTTCATATCCGGGCAT 786

Db 1353 ACTGAGGAGAGAGAGTGGTGGTTCAGCTGACGCCATATTTCATATCCGGGCAT 1412

QY 787 GACTGCATCCGACGCGAAGGAGCAGTTGTGCTTCTCAGAGACAAGTGCTCCATCCCT 846

Db 1413 GACTGCATCCGACGCGAAGGAGCAGTTGTGCTTCTCAGAGACAAGTGCTCCATCCCT 1472

QY 847 CCAATGACCAACAGACGATGCTGGAGAGCTGGCTCTCTTCTGTGCTGCTGTG 906

Db 1473 CCAATGACCAACAGACGATGCTGGAGAGCTGGCTCTCTTCTGTGCTGCTGTG 1532

QY 907 GCTGTGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 966

Db 1533 GCTGTGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1592

QY 967 ACGTCTTTCTTAATTTCCACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026

Db 1593 ACGTCTTTCTTAATTTCCACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1652

QY 1027 TCTGAGATATGTTTCCATCACACGCTGTGTGCTTCACTGACTGACTTCTTCAAACTACTGC 1086

Db 1653 TCTGAGATATGTTTCCATCACACGCTGTGTGCTTCACTGACTGACTTCTTCAAACTACTGC 1712

QY 1087 AGAAGTAGGTATCTCTTGAAGAAATGCGAAGAAATGCGGAGATGCGGCGGTA 1146

Db 1713 AGAAGTAGGTATCTCTTGAAGAAATGCGAAGAAATGCGGAGATGCGGCGGTA 1772

QY 1147 CAGTGGCTGACCACTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1206

Db 1773 CAGTGGCTGACCACTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1832

QY 1207 GTCCGAGCCTTTTGTGACAGTGTGCTGTGGCCCAATGAGGCGGAGGAGGAGGAGGAG 1266

Db 1833 GTCCGAGCCTTTTGTGACAGTGTGCTGTGGCCCAATGAGGCGGAGGAGGAGGAGGAG 1892

QY 1267 CAGGATCTGTTCCCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1326

Db 1893 CAGGATCTGTTCCCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1952

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Oy 1327 CTGCACAAATACCTGATGCTCTATCTTGGGGAGACAGCCTCAAGGCGACTATATATGCC 1386
    |||
Db 1953 CTGCACAAATACCTGATGCTCTATCTTGGGGAGACAGCCTCAAGGCGACTATATATGCC 2012
Oy 1387 CTGAGTGTCTGCCCCCAATATCATCTCATGAGAGAGCCACAGCTTTCCACACAGAACTT 1446
    |||
Db 2013 CTGAGTGTCTGCCCCCAATATCATCTCATGAGAGAGCCACAGCTTTCCACACAGAACTT 2072
Oy 1447 CTCAAGGCTACGACAGCATGTGAGTGAAGAAAGCTCAAGGCTGCTGATAGTGT 1506
    |||
Db 2073 CTCAAGGCTACGACAGCATGTGAGTGAAGAAAGCTCAAGGCTGCTGATAGTGT 2132
Oy 1507 TCACCCCTTGTAGTCCACCCGGGGAAATAGAGACTCTGAGCCTTCTACTCTCCCTTCCA 1566
    |||
Db 2133 TCACCCCTTGTAGTCCACCCGGGGAAATAGAGACTCTGAGCCTTCTACTCTCCCTTCCA 2192
Oy 1567 GTGACAAATGCTGTGTACAGACTCTGAAATGTGTGGAGAGGCTGTGTGAGTGTGCT 1626
    |||
Db 2193 GTGACAAATGCTGTGTACAGACTCTGAAATGTGTGGAGAGGCTGTGTGAGTGTGCT 2252
Oy 1627 ATGTACAAACCTGCTTTAAACCTGAGATTGCAAAAGTCAACCTGAGCATACGCTGAG 1686
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Db 2253 ATGTACAAACCTGCTTTAAACCTGAGATTGCAAAAGTCAACCTGAGCATACGCTGAG 2312
Oy 1687 GCTAGTCATTGGCTGAGATTATGAGACAAACAGATTACAGACATATATGATGGACCT 1746
    |||
Db 2313 GCTAGTCATTGGCTGAGATTATGAGACAAACAGATTACAGACATATATGATGGACCT 2372
Oy 1747 ACATTTGGGATATATCCCAAGCTGGGTATGATTAATCATGAGAACCAAGCCTGCGCC 1806
    |||
Db 2373 ACATTTGGGATATATCCCAAGCTGGGTATGATTAATCATGAGAACCAAGCCTGCGCC 2432
Oy 1807 ATGAAGTATATACGCGACTTCCCTGTCAGGCTGTCTGTCAGATTGGGCTCTTTCGACTG 1866
    |||
Db 2433 ATGAAGTATATACGCGACTTCCCTGTCAGGCTGTCTGTCAGATTGGGCTCTTTCGACTG 2492
Oy 1867 CCATGCTATGCTGACAGCTAGACCGCTTTTGAACATTTTATCTGTTAATGAATATATC 1926
    |||
Db 2493 CCATGCTATGCTGACAGCTAGACCGCTTTTGAACATTTTATCTGTTAATGAATATATC 2552
Oy 1927 CGTTTGGGAGCTCTCAAAAAAAAAAAAAAAAAAAAA 1963
    |||
Db 2553 CGTTTGGGAGCTCTCAAAAAAAAAAAAAAAAAAAAA 2589

RESULT 3
AADI2581
ID AADI2581 standard; cDNA, 1818 BP.
XX
AC AADI2581;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human protein having hydrophobic domain encoding cDNA clone HP10758.
XX
KW Human; hydrophobic domain; gene therapy; nutritional supplement;
KW cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
KW haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
KW contraceptive; antifertility; antiinflammatory; ss.
XX
OS Homo sapiens.
XX
FH key Location/Qualifiers
FT CDS 26..1534
FT /tag= a
FT /product= "Human protein having hydrophobic domain"
FT /note= "CDS is specifically is claimed in claim 3"
FT sig_peptide 26..70
FT mat_peptide 71..1531

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FT /tag= c
FT /product= "Mature human protein with hydrophobic domain"
XX
PN MO200149728-A2.
XX
PD 12-JUL-2001.
XX
PF 28-DEC-2000; 2000MO-JP09359.
XX
PR 06-JAN-2000; 2000JP-0000585.
XX
PR 06-JAN-2000; 2000JP-0000588.
XX
PR 11-JAN-2000; 2000JP-0002299.
XX
PR 03-FEB-2000; 2000JP-0026862.
XX
PR 03-MAR-2000; 2000JP-0058367.
XX
PA (PROT-) PROTEGENE INC.
PA (SAGA) SAGAMI CHEM RES CENT.
PI Kato S, Kimura T;
XX
PS WPI; 2001-418355/44.
XX
DR P-PDB; AAE06586.
XX
PT Human proteins with hydrophobic domains and the nucleic acids encoding
PT them, useful for preventing diagnosing and treating e.g. cancer,
PT Alzheimer's and inflammation.
XX
Claim 4; Page 340-344; 563pp; English.
XX
CC The present sequence is human protein with hydrophobic domain encoding
CC cDNA clone HP10758. The polynucleotide and polypeptide of the invention
CC may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The polynucleotides
CC may be used to produce the polypeptide, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the protein. The
CC polynucleotides and its complementary sequences may also be used as DNA
CC probes in diagnostic assays and also used in gene therapy. The
CC polypeptides may also be used as antigens in the production of antibodies
CC and in assays to identify modulators of polypeptide expression and
CC activity. The polypeptides and nucleic acids may be used as nutritional
CC supplements, to modulate cytokine and cell proliferation activity, to
CC modulate immune stimulation or suppression (e.g. for the treatment of
CC microbial infections and autoimmune disorders such as multiple sclerosis,
CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
CC haematopoiesis, to modulate tissue growth activity (e.g. for the
CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
CC disease), to modulate activin and inhibin activity (e.g. for controlling
CC fertility), to modulate chemotactic and chemokinetic activity, to
CC modulate haemostatic and thrombolytic activity, to modulate receptor
CC ligand activity, to modulate inflammation and to inhibit tumour growth.
XX
SQ Sequence 1818 BP; 522 A; 447 C; 404 G; 445 T; 0 other;

Query Match 50.4%; Score 989.8; DB 22; Length 1818;
Best Local Similarity 77.9%; Pred. No. 6.8e-293;
Matches 1249; Conservative 0; Mismatches 337; Indels 17; Gaps 4;

Oy 6 CAGTGGCGGGGCGATGCTGATGCTGATCTTGGCTGATGCTGAGAGAGGCCCT 65
    |||
Db 13 CAGTGGCGGGGCGATGCTGATGCTGATGCTGATGCTGAGAGAGAGGCCCT 72
Oy 66 GCCTGAGAGCCGACTATTCAGTGTGCTCTGAGACAGGGCCATCTCCAGAGTGTGT 125
    |||
Db 73 ACCCGAGAGCCGACCGTTCATGTGCTCTGAAACCTGGGCCATCTCCAGAGTGTGT 132
Oy 126 CCAACACACATCTACTCCAGAGACTTGAAGGACCTCCAGTGAACCTGCTCAAGCAAG 185
    |||
Db 133 ACAACATGATCTAATCCCGGAGACTTGAAGGACCTCCAGTGAACCTGCTCAAGCTAG 192
Oy 186 TGTGGAGAGAGAGATTTCATTTGATGAACATATAGCTGGAATCCGGGAGAGAGCC 245
    |||
Db 193 TGTTCACACAGGAGACTATTCATTTGATGAACATATAGCTGGAATCCGGGAGAGAGCC 252

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Qy	246	CAGATCCGCTGTGTTGAAGGCACAAAGATCTGCGGAGTGGCAAAAACAATGAAATTC	305
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Qy	306	ATACAGCTGTGTGAGTGCACCTACACAGAGGCGCTTCAAAGCCAGACACGACTTCCGG	365
Db	313	CTACAGCTGTGTGAGTGCACCTACACAGAGGCGCTTCAGACCTAGACACGACTTCCGG	372
Qy	366	CGGCAATTGACATTCTCTATGTAGGCTTCCCTGTGAGCTGAGACCTCTATATCAT	425
Db	373	TGTGTAATTGACATTCTCTATGTAGGCTTCCCTGTGAGCTGAGACACGACTTATTCAT	432
Qy	426	CAGGGCCCATPACATCCCAATGCTAATATGAAATGAGACAGCCCTTCTTCTCTGTAA	485
Db	433	TGGGGCCCATPATAATTTCTAATGAAATATGAAATGAGAGTGGCCCTTCATCTCTGTAA	492
Qy	486	CTTCAACCTGCGCAGGCTGCGCTTAACACAGTATGAAATATTAATAAAGCAGTGCATGAGGC	545
Db	493	TTTCACTCTACACAGGCTGCGCTTAACACAGTATGAAATATTAATAAAGTGTGTCAAGGC	552
Qy	546	GGGAGGCTGTGGGACCCAGACATCATCTGCTTGTAAAAAAGACGAGAGATGTTGAAGT	605
Db	553	CGGAAGCCTGTGGGATCCGAAATCATCTGCTTGTAAAAAAGATGAGAGACAGTGAAGT	612
Qy	606	GAATTTCAACAACCATCTCCCTTGGAAACAGATACAGATTTTCATTCAACGGGACACGAC	665
Db	613	GAATTTCAACAACCATCTCCCTTGGAAACAGATACAGATTTTCATTCAACAGGACATAT	672
Qy	666	ATTGGGGGTTTTCTAGAGTGCAGG-----AGAAATTAACATGATGAGGAGCTCTGTATGC	716
Db	673	CATCGGGTTTTCTAGAGTGTGTTAGCCACACCAAGAAACAAACCGAGCTTCAGTGT	732
Qy	717	CATCCCGGTGACTGAGAGAGTGAAGGTGCGGTGTTCACTGACGTGACCCCATATTTATCATAC	776
Db	733	GATTCACAGTACTGGGATGATGTAAGGTGCTACGGTGACAGCTGACCTCATATTTTCTCAC	792
Qy	777	CTGGGGCAATGATCTGCATCCGACGCCAAGGGAACAGTTTGTCTTGTCTGAGACAAATGTC	836
Db	793	TTTGAGCAGCACTGATCTCGACATAAAGGAAACAGTTGTGCTCTGCCCAAAACAGGGGT	852
Qy	837	TCCCATCCCTCAGATGACAAACAGACATGCTGGGAGGTGGCTGCGCTCTCTCTGAGT	896
Db	853	CCCTTTCCCTCTGATTAACAAACAAAGCAAGCCGGAGGCTGGCTGCTCTCTCTCTGCT	912
Qy	897	G---CTGCTGTGCTGT	953
Db	913	GTCCTGT	972
Qy	954	AAGGAGCAGAAAGCGTCTTTTCTTATTTTCAACATGCTCTGCCCCCTCATTAAGTCTCT	1013
Db	973	AAGGATCAAGAAAGCTTCTTTTCTA---CAACCACTACTGCCCCCATTAAGTCTCT	1029
Qy	1014	GTGTGTTTATTCCTCTGAGATATGTTTCCATGACACCAATTTGTTACTGAAATTTCT	1073
Db	1030	TGTGTGTTATTCCTCTGAGATATGTTTCCATGACACCAATTTGTTACTGAAATTTCT	1089
Qy	1074	TCAAAACTACTGACAGAGTACATCTTTGAAATGAGCAAGAAATGAAATGAGCGCA	1133
Db	1090	TCAAAACTACTGACAGAGTACATCTTTGAAATGAGCAAGAAATGAAATGAGCGCA	1149
Qy	1134	GATGGGCGGTACAGTGTGTGACCACTCAAGAGCAAGCGGCAGATTAAGTGTCTTCTCT	1193
Db	1150	GATGGGCTCAGT	1209
Qy	1194	TCTTCCAGTGAAGTCCCGAACCCCTTGTGACATGCTGTGTGTGTGTGTGTGTGTGTGT	1255
Db	1210	TCTTCCAGTGAAGTCCCGAACCCCTTGTGACATGCTGTGTGTGTGTGTGTGTGTGTGT	1269
Qy	1254	CAGGAGAACTCTCAGAGATCTGTTCCTCTGTGCTTTAACTCTTTTGTAGTGAATTTGAG	1313
Db	1270	CAGTGAAGAACTCTCAGAGATCTGTTCCTCTGTGCTTTAACTCTTTTGTGAGTGAATTTGAG	1329
Qy	1314	CAGCGAAGCATCTGCAACAATATCTGTGTGTATCTTGGGGGAGCAGACCTCAAGG	1373

Accession	Sequence	Position
Dh	1330 AAGCGAATTCATCTGCAAAATACGTGGTGTCTACTTTAGAGAGATGTATACAAAAGA	1389
Qy	1374 CGACTATATATGCCCTGAGTCTGCCCCCAATATATCTCATGAAGACGCCACACTTT	1433
Dh	1390 CGATTACAAATGCTCTCAGTCTCTGCCCCAAGTACCACTCATGAAGAGATGCCATGCTTT	1449
Qy	1434 CCACACGAATCTTCTCAAGGCTACGAGAGCATGTGTAAGAAAGCTCATCAAGCTG	1493
Dh	1450 CTGTGCGAAATCTCTCCATCTCAAGCAGCAGAGGTGTGAGAGAAAATATACAAAGCTG	1509
Qy	1494 CCATGATAGCGTTTCAACCTTGAAGTCCACCGGGGAAA--TAGAGACTGGAAGCCTT	1551
Dh	1510 CCAAGATGGTGTGCTGCTCTTTTGAAGCCACCATATAGAAAGCAAGAGACTTTAAAGGCTTC	1559
Qy	1552 CTACTCTCTCTTCCAATGACAAATGCTGTGTACACACTGTAA	1594
Dh	1570 CTATCCCAACCAATTCACGGAAGAAAACGTGTATATATCTGTAA	1612

Result 4	ID	Accession	Standard	DNA	Length
AD28776	AD28776	standard	DNA	1841 BP	
AD28776	AD28776				
07-MAY-2002	(first entry)				
Human Interleukin-17 receptor B-2 (IL-17RB-2)	DNA				
Human, interleukin-17 receptor B-2; IL-17RB-2; immune system dysfunction; cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus; inflammatory bowel disease; neuronal dysfunction; transplant rejection; autoimmune disorder; lung; skin; kidney; bone; eye; vascular system; infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis; cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema; eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease; epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis; leukaemia; retinal neuropathy; infertility; miscarriage; inflammation; cancer; diabetes; ds.					
Homo sapiens.					
Key	Location/Qualifiers				
CDS	50..1558				
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	/product= "Human IL-17RB-2 protein"				
sig_peptide	50..92				
	/*tag= b				
mat_peptide	93..1555				
	/*tag= c				
	/product= "Mature IL-17RB-2 protein"				
WO200208285-A2.					
31-JAN-2002.					
21-JUN-2001; 2001WO-US19861.					
22-JUN-2000; 2000US-213125P.					
02-FEB-2001; 2001US-266159P.					
16-MAR-2001; 2001US-0810384.					
(AMGE-) AMGEN INC.					
Medlock E, Yeh R, Silbiger SM, Elliott GS, Nguyen HQ, Jing S;					
WPI; 2002-155217/20.					
P-PSDB; AAB18127.					
Nucleic acid molecules encoding interleukin 17 (IL-17) - like					
polypeptides useful in the treatment, prevention and diagnosis of					
diseases e.g. cancer					

XX Disclosure; Page 230-232; 242p; English.
 XX The invention relates to nucleic acid molecules encoding Interleukin 17
 XX (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels
 XX of IL-17 protein in an animal. The IL-17 protein is useful for treating,
 XX preventing or ameliorating a disease, such as immune system dysfunction
 XX (rheumatoid arthritis, osteoarthritis, inflammatory joint disease),
 XX autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel
 XX disease, transplant rejection, graft vs. host disease), infections (HIV,
 XX hepatitis, bacterial), weight disorders (obesity, anorexia, cachexia,
 XX sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung
 XX (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin
 XX (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone
 XX (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy
 XX atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma
 XX leukemia); reproductive (infertility, miscarriage, endometriosis), eye
 XX (blindness, retinal neuropathy) and treatment of diseases involving
 XX inflammation. The present sequence is human Interleukin-17 receptor B-2
 XX (IL-17RB-2) DNA.

SO Sequence 1841 BP; 522 A; 455 C; 416 G; 448 T; 0 other;

Query Match 50.3%; Score 988.2; DB 24; Length 1841;
 Best Local Similarity 77.9%; Pred. No. 2.1e-292;
 Matches 1248; Conservative 0; Mismatches 338; Indels 17; Gaps 4;

QY 6 CAGTGGCCGGGCGATGTTGCTAGTGTGCTGATCTTGGCTGCATCCGCGAGAGCGCCCT 65
 DB 37 CAGTGGCCGGGCGATGTTGCTAGTGTGCTGATCTTGGCTGCATCCGCGAGAGCGCCCT 96
 QY 66 GCCTCGAGAGCGGAGTATTCAGTGTGCTCTGAGACAGGCGCATCTTCAGAGTGTAGTGT 125
 DB 97 ACCCGGAGAGCGGAGTATTCAGTGTGCTCTGAGAACTGGGCGCATCTTCAGAGTGTAGTGT 156
 QY 126 CCAACACACACTCACTCAGAGAGACTTGAGGAGCTTCAAGTGAAGTCTCTCAAGACAG 185
 DB 157 ACAACATGATCTATCCCGAGAGCTTGAGGAGACTTCCGAGTGAACCTTTTCAACTAG 216
 QY 186 TGTGGCAGCAGAGAGATTTTCAATTTGATGAACATTAAGTGTGATCTCCGGGAGAGCG 245
 DB 217 TGTGGCAGCAGGAGATTTTCAATTTGATGAACATTAAGTGTGATCTCCGGGAGAGTGC 276
 QY 246 CAGCATCCGCTTGTGAAGGCAACAGATCTGCTGAGTGTGAGCAAAACAACTGAATTC 305
 DB 277 CAGCATCCGCTTGTGAAGGCAACAGATTTTGTGTAAGGCAAAACAACTTCCAGTTC 336
 QY 306 ATTCAGCTGTGTGAAGTGTCACTACACAGAGGCTTCAAGCCAGACAGACCTTCCGG 365
 DB 337 CTACAGCTGTGTGAAGTGTCACTACACAGAGGCTTCCAGACTCAGACAGACCTCTGG 396
 QY 366 CGGCAATGAGCATCTTCCATGATGAGGCTCCCTGTGAGCTAGAGCACTCTATCTCAT 425
 DB 397 TGTGAATGAGCATTTTCTTCACTGAGGCTTCCCTGTGAGCTAGAGCACTCTATTTTCAT 456
 QY 426 CAGCGCCATTAATCCCATGATGATGAATGAAGAGAGCGCTTCTTGTCTGTGA 485
 DB 457 TGGGGCCCAATATTTCTTATGATGAATGATGAAGATGGCCCTTCCATGCTGTGAA 516
 QY 486 CTTCACCTCGCCAGGCTGCTTAAACAGTAATGAATATTAAGAGAGTGAAGG 545
 DB 517 TTTACACCTCAAGGCTGCTTAAACAGTAATGAATATTAAGAGAGTGAAGG 576
 QY 546 GGAAGCGCTGTGAGAGCCAGACATCACTGTTTAAATAAGAGAGATGTTGAAGT 605
 DB 577 CGAAGCGCTGTGAGAGCCAGACATCACTGTTTAAATAAGAGAGATGTTGAAGT 636
 QY 606 GAATTTACAAACCAATCCCTTGGAAACAGATACAGATCTCTCATTCAGAGGAGACAG 665
 DB 637 GAATTTACAAACCAATCCCTTGGAAACAGATACAGATCTCTCATTCAGAGGAGACAG 696
 QY 666 ATTTGGGCTTTCTAGAGTGTG-----AGATTAACATGATGAGAGCTGTGAGC 716

DB 697 CATCGGCTTTCTCAGTGTGTTGAGCCACACAGAAAGAAACGAGCTTCACTGCT 756
 QY 717 CATCCGGTGAAGTGAAGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 776
 DB 757 GATTCAGTGAAGTGAAGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 816
 QY 777 CTGCGCAATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 836
 DB 817 TGTGACAGAGTGAAGTGAAGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 876
 QY 837 TCCCATCCCTCCAGATGACACAGAGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 896
 DB 877 CCTTTCTCTGAGTGAAGTGAAGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 936
 QY 897 G---CTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 953
 DB 937 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 996
 QY 954 AAGAGCAGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1013
 DB 997 AAGATCAAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1053
 QY 1014 GGTGCTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1073
 DB 1054 TGTGCTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113
 QY 1074 TCAAACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1133
 DB 1114 TCAAACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1173
 QY 1134 GATGGGCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1193
 DB 1174 GATGGGCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1233
 QY 1194 TCTTCCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1253
 DB 1234 TCTTCCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1293
 QY 1254 CAGGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1313
 DB 1294 CAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1353
 QY 1314 CAGCAGAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1373
 DB 1354 AAGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1413
 QY 1374 CGACTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1433
 DB 1414 CGACTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1473
 QY 1434 CCAACAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1493
 DB 1474 CTGTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1533
 QY 1494 CCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1551
 DB 1534 CCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1593
 QY 1552 CTACTCTCCCTTCCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1594
 DB 1594 CTATCCCACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1636

RESULT 5
 ABA03200
 ID ABA03200 standard; cDNA; 1841 BP.
 XX
 AC ABA03200;
 XX
 DT 11-FEB-2002 (first entry)
 XX
 DE Human IL-17 receptor like protein #1 coding sequence.
 XX

Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic; antipsoriatic; antimicrobial; anorectic; nocotropic; neuroprotective; antiaschemic; antiallergic; dermatological; cytoskeletal; gene therapy; interleukin 17; immune system disorder; infection; weight; reproductive; neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation; glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye; tumour; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 50..1558
FT /tag= a
FT /product= "Human IL-17 receptor-like protein #1"

MO200168705-A2.

20-SEP-2001.

16-MAR-2001; 2001WO-US08688.

16-MAR-2000; 2000US-189923P.
PR 12-MAY-2000; 2000US-204208P.
PR 27-NOV-2000; 2000US-0722232.
PR 02-FEB-2001; 2001US-266159P.

(AMGE-) AMGEN INC.

Jing S, Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ.
WPI: 2002-055100/07.
P-PSDB; AAM47456.

Three human nucleic acids encoding interleukin 17 (IL-17) receptor like polypeptides, useful for treating, diagnosing, ameliorating or preventing immune system disorders (e.g. psoriatic arthritis) and infections (e.g. viral infections)

Claim 1; Fig 1; 239pp; English.

The present invention relates to novel human nucleic acids encoding interleukin 17 (IL-17) receptor like proteins. The present sequence is one such coding sequence. The IL-17 receptor-like proteins and coding sequences are useful for treating a pathological condition related to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g. viral infections), weight disorders (e.g. obesity), neuronal dysfunction disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis), bone disease (e.g. osteoporosis), vascular system disorders (e.g. ischaemia), eye disorders, reproductive disorders, tumours and inflammation.

Sequence 1841 BP; 522 A; 455 C; 416 G; 448 T; 0 other;

Query Match 50.3%; Score 988.2; DB 24; Length 1841;
Best Local Similarity 77.9%; Pred. No. 2.1e-292;
Matches 1248; Conservative 0; Mismatches 338; Indels 17; Gaps 4;

6 CAGTGGCCGGGCGCATGTTGCTAGTGTGCTGATCTTGGCTGATGCTGAGAGAGCCCT 65
Db 37 CAGTGGCCGGGCGCATGTTGCTAGTGTGCTGATGCTTGGCTGAGAGAGCCCT 96

66 GCGTGGAGAGCGGACATGCTGAGTGGCTCTGAGACAGGGCCATCTCCAGAGTGAATGT 125
Db 97 ACCCGAGAGCGGACGCTTCAATGAGCTCTGAACTGGGCGCATCTCCAGAGTGAATGT 156

126 CCAACACACACTCACTCCAGAGACTTGAAGGACCTCCAGTGAACCTGTCAGAGCAAG 185
Db 157 ACAACATGATTAATCCCGGAGACTTGAAGGACCTCCAGTGAACCTGTCAGAGCAAG 216

186 TGTGGCAGAGAGAGATTTTCAATTTTGAATGAACATTAAGTGAATCTCCGGGAGAGCC 245
Db 217 TGTTCGAACAGGAGGACTTAATTTTGAATGAATGAATGAATGAGTGAATCTCCGGGAGAGATGC 276

246 CAGCATCCGCTTGTGAAAGGCCAACAGATCTGCGTAGTGCGCAAAAACAATGAATTC 305
Db 277 CAGCATCCGCTTGTGAAAGGCCAACAGATTTGTGAGAGGGGAAAAGCACTTCCAGTC 336

306 ATACAGCTGTGTGAGGTGCACTACACAGAGGCTTCCAAAGCCAGACAGACCTTCCG 365
Db 337 CTACAGCTGTGTGAGGTGCAATTAACAGAGGCTTCCAGACTCAGACCAAGCCCTCG 396

366 GGGCAATGAGATTCCTGATGAGGCTTCCGTGAGGCTGAGAGCTGATCTGATCT 425
Db 397 TGTAAATGAGATTCCTGATGAGGCTTCCGTGAGGCTGAGAGCTGATCTGATCT 456

426 CAGCGCCCAATCAATCCCAATGATTAATGATGAGAGACAGCCCTTCTTGTCTGAA 485
Db 457 TGGGGCCCAATTAATTCCTAATGCAATGATGATGAGAGTGGCCCTTCATGCTGAA 516

486 CTTCACCTGCGCAGGCTGCTTAACCAAGTAATGAATTAATAAGACAGTGCATGAGC 545
Db 517 TTTCACTTCAACAGGCTGCTTAACCAAGTAATGAATTAATAAGACAGTGCATGAGC 576

546 GGGAGGCTGTGGGACCCAGACATCACTGCTGTAATAAAGAAAGAGATGTTGAGT 605
Db 577 CGAAGCTGTGGGATCCGAACATCACTGCTGTAATAAAGAAAGAGAGACAGTGAAGT 636

606 GAATTTCAACAACCAATCCCTTGGAAACAGATACAGATTCATTCATTCAGGAGACAG 665
Db 637 GAATTTCAACAACCAATCCCTTGGAAACAGATACAGATTCATTCATTCAGGAGACAG 696

666 ATTTGGGTTTCTTAAGATGCTGG-----AGATAAATGATGAGAGCGTCTGTAGC 716
Db 697 CATCGGTTTCTCAGAGTGTGAGGACCAACCAAGAAAGCAAGCGGAGCTTCAAGTGT 756

717 CATCCCGGATGAGAGAGAGAGAGAGGAGGAGTGGCTGACGCTGACCCCATTTATCATC 776
Db 757 GATTCAGAGTGGGAGATGAGAGGAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGGAG 816

777 CTGGGCAATGACTGATCCGACGAGAGGAGCAGTGTGCTTGTCTGAGACAGAGTCC 836
Db 817 TTGTGGCAGCAGCTGATCCGACATTAAGAGACAGTGTGCTGCTGCTGCTGCTGCTGCT 876

837 TCCCATCCCTCCAGATGACCAACAGAGAGTGTGGAGGCTGCTGCTGCTGCTGCTGCT 896
Db 877 CCCTTCCCTCGATTAACCAACAGAGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCT 936

897 G---CTGCTGT 953
Db 937 GTCTGT 996

954 AAGAGCAGAAAGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1013
Db 997 AAGATCAAGAAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1053

1014 GGTGTTTATCTTCTGAGATATGTTTCCATGACACCGTCTGCTGCTTCTTCTTCTTCT 1073
Db 1054 TGTGTTTATCTTCTGAGATATGTTTCCATGACACCAATTTCTTCTTCTTCTTCTTCT 1113

1074 TCAAAATCTACGAAATGAGTGTATCTTGAATAAATGCGAATAAATGCGCA 1133
Db 1114 TCAAAATCTACGAAATGAGTGTATCTTGAATAAATGCGAATAAATGCGCA 1173

1134 GATGGGCGGATACAGT 1193
Db 1174 GATGGGCGGATACAGT 1233

1194 TCTTCCAGTGAAGTCCGACCTTGTGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1253
Db 1234 TCTTCCAGTGAAGTCCGACCTTGTGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1293

1254 CAGGAGAACTCTCAGATCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1313
Db 1294 CAGTGAAGAACTCTCAGATCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1353

QY	964	AAGAGCTCTTTCCTATTTTCCACCAAGTCTCTCCCTCATTAAGGTCGTGGTGTAT	10233
Db	961	AAGACTTCCTTTTCTA---CCACCAACTACTCTCCCCCATTAAGGTTCTTGCTGTTTAC	10178
QY	1024	CTTCTGAGATATGTTTTCATCAACCGTCGTGCTTCACTGACTTTTCTTCAAAATAC	10833
Db	1018	CCATCTGAAATATATGTTTCCATACACAAATTTGTTACTTCACTGAATTTCTTCAAAACAT	10777
QY	1084	TGCAGAACTGAGGTCATCTCTTGGAAAAATGGCAGAAAAAAGAAATGCGCGAATGGGGCG	11433
Db	1078	TGCAGAAATGAGGTCATCTTGGAAAAATGGCAGAAAAAAGAAATGACAGATGGGTCCA	11373
QY	1144	GTACAGTGGCTGACCACTCAAGAACGAGGGGAGATAAAGTGTCCTCTTCTCCCACT	12033
Db	1138	GTCAGTGGCTTGGCACTCAAAAGAGGACAGACAAAGTCGTCTTCTCTTTCAT	11973
QY	1204	GACGTCGCACTCTTGTGACAGTGCTGTGGCCACATGAGGGCAGCGCCAGGAGAAC	12633
Db	1198	GACGTCAAAGTGTGTGTCGATGTGACTGTGGCAAGGAGGGCAGTCCAGTAGAAC	12573
QY	1284	TCTCAGGATCTGTTTCCTCTTGGCTTTACCTCTTTTGTAGTGAATTCAGACGCAACG	13233
Db	1258	TCTCAAGACTCTTCCCCCTTGGCTTTAACCTTTTCTGCAGTGATCTAGAAGCCAGATT	13173
QY	1324	CATCTGACAAATCTCGTGTCATCTTTGGGGGACAGACCTCAAAAGCGACTATAT	13833
Db	1318	CATCTGACAAATACGTTGGTCTACTTTAGAGATTTGATACAAAGACGATTTACAT	13773
QY	1384	GCCCTGAGTGTCTGCCCCCAATATCATCTCATAGAGACCCACAGCTTTCACACAGAA	14433
Db	1378	GCTCTCAGTGTCTGCCCCCAAGTACACTTATAGAGATGCCACTGCTTTCTGTGACAGAA	14373
QY	1444	CTTCTCAAGGCTGACGAGACATGTACGTGAMAAAAAGCTCAACAGCTTCAGTATAGC	15033
Db	1438	CTTCTCAGTGTGACGAGACAGGTGTACGACGAAAAAAGATCAACAGCTGCCACATGCG	14973
QY	1504	TGTTCAACCTTTGATGTCCACCCGGGGGAA--TGAGACTCTGAAGCTTCTTACTCTCC	15613
Db	1498	TGCTGCTCTTGTAGCCCACTCATGAGAACAGAACCTTTAAAGGCTTCTACTCCACC	15573
QY	1562	TTCCAGTGACAAATGCTGTGTCGACTGTGAA	1594
Db	1558	AATTACAGGAAAAAACGTGTGATGATCTTGA	1590
RESULT 7			
AAH99008			
ID	AAH99008 standard; cDNA; 2161 BP.		
XX	AAH99008;		
AC	12-OCT-2001 (first entry)		
XX	Human EST-derived coding sequence SEQ ID NO: 865.		
DE	Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;		
XX	tomato; monkey; dog; sea urchin; expressed sequence tag; EST;		
KW	diagnostics; forensic test; gene mapping; genetic disorder;		
KM	biotechnology; gene therapy; nutrition; ss.		
XX	Homo sapiens.		
OS	WO200154477-A2.		
PN	02-AUG-2001.		
XX	25-JAN-2001; 2001WO-US02687.		
PD	25-JAN-2000; 2000US-0491404.		
XX	17-JUL-2000; 2000US-0617746.		
PR	03-AUG-2000; 2000US-0631451.		
PR	15-SEP-2000; 2000US-0663870.		

PA	(HYSE)-HYSEQ INC.
XX	
PI	Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI	Cao Y, Drmanac RA, Zhang J, Weirman T;
XX	
XX	WPI; 2001-476164/51.
DR	P-PSDB; AAM24349.
XX	
PT	Isolated polypeptide for treatment of diseases, diagnostics, raising
XX	antibodies and research use -
PS	
XX	Claim 1; Page 707; 1275pp; English.
CC	
CC	The present invention provides the protein and coding sequences of novel
CC	proteins from a variety of organisms, including human, dog, cat, horse,
CC	cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC	urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC	from the organism of interest. They can be used in diagnostics,
CC	forensics, gene mapping, identification of mutations, to assess
CC	biodiversity and for nutritional purposes. The present sequence is a cDNA
CC	of the invention.
SQ	Sequence 2161 BP; 639 A; 516 C; 446 G; 560 T; 0 other;
Query Match	50.0%; Score 982.4; DB 22; Length 2161;
Best Local Similarity	77.9%; Pred. No. 1,4e-290;
Matches 1241; Conservative	0; Mismatches 336; Indels 17; Gaps 4;
OY	15 GGCCATGTTGTCTAGTGGTCGATCTTGAGCGCATCGTAGCAGAGCGGCCCTGCCTCGAGA 74
Db	4 GCCATGTGCGCTCGTCTTAAGCCTGACCGCGCTGTGCAAGAGCGCCGTAACCCCGAGA 63
OY	75 GCCGACTATTGACGTGTGCTCTGACACAGGGCCATCTCCAGAGTGATGGTCCAAACAC 134
Db	64 GCCGACCGTTCAATGTGCTGTGAACCTGGGCCATCTCCAGAGTGATGGTCCAAACATGA 123
OY	135 ACTCACTCAGAGCACTTGAGGAGCTTCCAGTGAATCTGTCAAGACAAGTGTGGCAC 194
Db	124 TCTAATCCCCGGAGACTTGAAGGACCTCCGATGAACCTGTATCAACTAGTGTGCAAC 183
OY	195 AGAGAGTTTTCAATTTGATGATGAACATAAGCGGATATCTCCGGGCGAGCGCAGCATCCG 254
Db	184 AGGGACATATTCATTTGATGATGAATGTAAAGCTGGGTACTCCGGGCGAATGCCAGCATCCG 243
OY	255 CTGTGTAAGGCCAACCAAGATCTGGCTAGTGGCAAAAACAAACATGAATTCAACAGCTG 314
Db	244 CTGTGTAAGGCCAACCAAGATTTGTGTGACGGGGCAAAAGCAAATCTCAGTCTCAAGCTG 303
OY	315 TGTCAGTGCAACTACACAGAGGCTTCCAAAGCCAGCCAAGACTCTCCGGCGCAATG 374
Db	304 TGTCAGTGCAATTAACAGAGGCTTCCAACTCAGACCAGACCTCTGGGTGTAATAG 363
OY	375 GACATTTCTTATGTAAGGCTTCCCTGTGAGCTGAGCACTCTATCTCATACAGGCCCA 434
Db	364 GACATTTCTTCAACATCGGCTTCCCTGTGAGCTGAAACAAGCTAATTTCAATGGGGCCA 423
OY	435 TAACATCCCAGATGTATATGAATGAAGAGCAGCGCTTCTTGTGTGGAATTCACCTC 494
Db	424 TAAATTTCTTATGTAAGTAATGAATGAAGAGGCGCTTCCATGCTGTGTAATTTCACTC 483
OY	495 GCCAGGCTGCTAAACAACGTAATGAATATMAAAGCAGTGCACTGAGGGCGGAAGCT 554
Db	484 ACCAGGCTGCTTAAGCCACATATGAATATMAAAGTGTGTCALAGGGCGGAAGCT 543
OY	555 GTGGGACCCAGACATCATCTGCTTGTAAAAAGAGCAAGAGATGTTGAATGAATTTCAAC 614
Db	544 GTGGGATCCGAACATCATCTGCTTGTAAAAAGATGAAGAGCAAGTAAGTAATTTCAAC 603
OY	615 AACCAATCCCTTGGAAACAGATACACGATTTCTCATTAACGGGACAGACATTTGGGGTT 674
Db	604 AACCACTCCCTTGGAAACAGATACATGAGCTTTTATCCAAACAGACATTAATCATGGGTT 663
OY	675 TTCTAGAGTGTGTG-----AGATTAACATGATGAGAGCTCTGAGCATCCCGGT 725

[illegible]

XX	Human; interleukin-17 receptor related protein; IL-17; chromosome 3p21; EVI27; retroviral integration; chromosomal mapping; mutational analysis; BXI2 murine myeloid leukaemia; proinflammatory cytokine; IL-8; therapy; haematopoietic cell; cancer; autoimmune disease; ss.
XX	Homo sapiens.
XX	Key
XX	Location/Qualifiers
XX	6..1514
XX	/tag= a
XX	/product= "Human EVI27 protein"
XX	6..44
XX	/tag= b
XX	45..1511
XX	/tag= c
XX	/product= "Human mature EVI27 protein"
XX	WO200157202-A2.
XX	09-AUG-2001.
XX	02-FEB-2001; 2001WO-US03518.
XX	04-FEB-2000; 2000US-0180374.
XX	(UYAR-) UNIV ARKANSAS.
XX	Shaughnessy JD;
XX	WPI; 2001-496920/54.
XX	P-PSDB; AA07160.
XX	New nucleic acids encoding an interleukin (IL)-17 receptor related protein for use as a marker for leukemia -
XX	Claim 1a; Page 74-75; 87pp; English.
XX	The present sequence is a cDNA encoding human interleukin (IL)-17 receptor related protein (EVI27). Human EVI27 gene was mapped to chromosome 3p21. EVI27 is a common site of retroviral integration in BXI2 murine myeloid leukaemia. EVI27 cDNA sequences are useful as antisense molecules to inhibit EVI27 protein or for chromosomal mapping or mutational analysis of EVI27 protein. They are proviral integration sites associated with leukaemias and monitoring this site provides a genetic tag for disease gene identification. The proteins of the invention are useful to stimulate the secretion of proinflammatory cytokines such as IL-8 and plays an important role in the developmental and/or disease processes of haematopoietic cells. Hence modulating the expression of EVI27 at the RNA or protein level is used in the treatment of diseases such as cancer or autoimmune diseases.
XX	Sequence 1827 BP; 547 A; 438 C; 397 G; 445 T; 0 other;
XX	Query Match 50.0%; Score 980.8; DB 22; Length 1827;
XX	Best Local Similarity 77.8%; Pred.No. 4e-290;
XX	Matches 1240; Conservative 0; Mismatches 337; Indels 17; Gaps
XX	15 GGCATGTTGCTAGTGTTCGATCTTGGCTGCATCGTCGAGAGCGCCCTGCTGAGA 74
XX	2 GGCATGTCGCTCGTCGATGATGAGCTGCGCGCTGTGACAGAGCGCCGTAACCCGAGA 61
XX	75 GCCGACTATTCAGTGTGACTCTGAGACAGAGGCGCATCTCCAGAGTGATGATCAACACAC 134
XX	62 GCCACCGCTTAAATATGTGCTCTGAACACTCGGCGCATCTCCAGAGTGATGATCAACATGA 121
XX	135 ACTCACTCCAGAGAGCTTGAGGAGACTTCAAGTGAATCTGTCAGACAGATGTGGCAGC 194
XX	122 TCTATCCCGGAGACTTGAAGGAGCTCCGAGTGAACCTGTTAACAATGATGTGCAAC 181
XX	195 AGAGAGTTTTCATTTGATGAAACATAGCTGATCTCCGGGCAAGCGCCAGATCCG 254

XX Sequence 1918 BP; 560 A; 469 C; 426 G; 461 T; 2 other;
 SQ Query Match 49.5%; Score 970.8; DB 21; Length 1918;
 Best Local Similarity 77.8%; Pred. No. 4.8e-287;
 Matches 1241; Conservative 0; Mismatches 337; Indels 18; Gaps 5;

13 CGGGCCATGTTGCTAGTGTGCTGATCTTGGCTGATGTCGACAGAGCGCCCTCGA 72
 105 CGAGCGATGTCGCTCGTGTCTTAAGCTGGCCGCGCTGACAGAGCGCCGTACCCCGA 164
 73 GAGCGCATTTTCAGTGTGCTGAGACAGAGGCAATCTCCAGAGTGTGTCCAAAC 132
 165 GAGCGGACCGTTCAATGTGTGTGAAACTGGGCAATCTCCAGAGTGTGTCCAAAC 224
 133 ACATCTCTCAGAGAGCTTGAGGAGACTCCAGTGGAACTCCGACAGCAAGAGTGGCA 192
 225 GATCTAATCCCGAGACTTGAGGAGCTCCAGTGAACCTGTTACAACTAGTGTGCA 284
 193 GCAGAGAGTTTTCATTTTGTATGATGATGATGATGATGATGATGATGATGATGATG 252
 285 ACAGGGGACTATTCAATTTTGTATGATGATGATGATGATGATGATGATGATGATGATG 344
 253 CGCTTTGTAAGGCAACAGATGTCGTGATGTCGCAAAACAAATGAAATTCATACAGC 312
 345 CGCTTTGTAAGGCAACAGATGTCGTGATGTCGCAAAACAAATGAAATTCATACAGC 404
 313 TGTGTGAGTGAACCTACAGAGAGCTTCCAAAGCCAGACCAAGCTTCCGCGGGGAAA 372
 405 TGTGTGAGTGAACCTACAGAGAGCTTCCAAAGCCAGACCAAGCTTCCGCGGGGAAA 464
 373 TGAACATTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 432
 465 TGAACATTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 524
 433 CATTAATCTCCCAATGCTATATGATGATGATGATGATGATGATGATGATGATGATG 492
 525 CATTAATCTCCCAATGCTATATGATGATGATGATGATGATGATGATGATGATGATG 584
 493 TCGCAGAGCTGCTTAACCAAGTGAATATTAAGAAAGCACTGAGAGGGGGGAAAGC 552
 585 TCACACAGGCTGCTTAACCAAGTGAATATTAAGAAAGCACTGAGAGGGGGGAAAGC 644
 553 CTGTGGAGCCAGACATCACTGCTTGTAAAGAAAGCAAGATGTTGAAGTGAATTTTC 612
 645 CTGTGGAGCCAGACATCACTGCTTGTAAAGAAAGCAAGATGTTGAAGTGAATTTTC 704
 613 ACAACCAATCTCCCTTGGAAACAGATACAGATTTCTTCAACGGGACAGCATTTGGGG 672
 705 ACAACCAATCTCCCTTGGAAACAGATACAGATTTCTTCAACGGGACAGCATTTGGGG 764
 673 TTTTCTAGAGTGTGCG-----AGAATAAAGTGAAGAGCTGTAGAGCATCCCG 723
 765 TTTTCTAGAGTGTGCGCAACCAAGAAAGCAAGCTGTAGAGTGAATTTCA 824
 724 GTGACTGAGAGAGTGAAGTGTGCGTGTCAAGTGAAGCTTCAATTTTCAATTCAGTGGC 783
 825 GTGACTGAGAGAGTGAAGTGTGCGTGTCAAGTGAAGCTTCAATTTTCAATTCAGTGGC 884
 784 AATGACTGATCCGAGCGGAGAGGAGAGTGTGCTTGTCAAGAGCAAGTGTCCCATC 843
 885 AGGACTGATCCGAGCACTAAGAGAGAGTGTGCTTGTCCACAAACAGAGCTCCCTTTC 944
 844 CCTCCAGATGACAAAGAGAGAGCTGTGAGAGCTGTGCTTCTTCTCTGGG---CTG 900
 945 CCTCCAGATGACAAAGAGAGAGCTGTGAGAGCTGTGCTTCTTCTCTCTGGG---CTG 1004
 901 CTGCTGCTGTGTGAGTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGAGAGAGC 960
 1005 CTGCTGCTGTGTGAGTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGAGAGAGC 1064
 961 ACGAAGAGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020

Db 1065 AAGAGACTTCTTTTCTA---CCACCACATAGCCCCCATTAAGGTTCTTGTGTT 1121
 Qy 1021 TATCTCTTGAAGATATGTTTCCATTCACACCGATGTCGCTTCACTGATTTCTTCAAAAC 1080
 Db 1122 TACCATCTGAATATGTTTCCATTCACACATTTGTTACTTACTGATTTCTTCAAAAC 1181
 Qy 1081 TACTGAGAGAGTGAAGTCACTCTTGAAGAAATGACAGAAAGAAATTCGCCAGATGGGG 1140
 Db 1182 CATTCAGAGAGTGAAGTCACTCTTGAAGAAATGACAGAAAGAAATTCAGAGATGGGT 1241
 Qy 1141 CCGTCAAGAGTGAAGTCACTCTTGAAGAAATGACAGAAAGAAATTCAGAGATGGGT 1200
 Db 1242 CAGTCAAGAGTGAAGTCACTCTTGAAGAAATGACAGAAAGAAATTCAGAGATGGGT 1301
 Qy 1201 AGTGAAGTCCCGACCTTTTGTGACAGTGTGCTGACATGAGAGGACGCGCAGAGAG 1260
 Db 1302 AATGAGTCAAGAGTGTGTCATGATGATGATGATGATGATGATGATGATGATGATG 1361
 Qy 1261 AACTCTAGAGATGTTTCCCTTGTGCTTTTAACTCTTTTGTGATGATTTTCAAGAGCCAG 1320
 Db 1362 AACTCTCAAGA-CTTTCCTCCCTTGTCTTTAACCTTTTCTGAGTGTATGAAGAGCCAG 1420
 Qy 1321 ACGCATCTGACAAATTAACCTGTGTGTCTATCTTTGGGGAGAGAGCTCAAGAGCCATAT 1380
 Db 1421 ATTCATCTGACAAATTAACCTGTGTGTCTATCTTTAGAGATTTGATCAAAAGAGATTAAC 1480
 Qy 1381 AATGCCCTGAGTGTGCTGCCCCCAATTCATCTCATGAAGAGAGCCAGCTTTTCCACACA 1440
 Db 1481 AATGCTCTAGTGTGTGCCCCCAATTCATCTCATGAAGAGAGCCAGCTTTTCTGTGCA 1540
 Qy 1441 GAACTTCTGAAGCTTACGAGAGAGATGATGATGAAGAAAGCTCAACAGCTTCCATGAT 1500
 Db 1541 GAACTTCTCAATGTCAAGTGAAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1600
 Qy 1501 AGCTGTTCACCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1558
 Db 1601 GGTGTGTCTCTTGTGAGCCACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1660
 Qy 1559 CCCTTCAGTGAAGATGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1594
 Db 1661 ACCAATTAAG 1696

RESULT 10
 AA52046
 ID AA52046 strand; cDNA; 1918 BP.
 XX
 AC AA52046;
 XX
 DT 09-AUG-2000 (first entry)
 XX
 DE cDNA encoding interleukin 17-like receptor protein (IL17RLP)-2.
 XX
 KW Interleukin-17-like receptor protein; IL-17RLP; cytokine receptor;
 KW resistant chronic infection; acute infection; mycobacterial infection;
 KW T-cell proliferation; IL-2 biosynthesis; lymphocytic leukaemia;
 KW T-cell mediated autoimmune disease; hematopoiesis; sepsis; hybridoma;
 KW IL-6 expression; myeloma; plasmacytoma; Lemmer's lymphoma;
 KW Immunoprotective; cytosolic; hematopoietic; proliferative;
 KW antibacterial; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 111..1412
 FT /*tag= a
 FT /product= "Interleukin-17 like receptor protein"
 XX
 PN MO200015759-A1.
 XX
 PD 23-MAR-2000.
 XX
 PF 15-SEP-1999; 99WO-US21048.

Db 1661 ACCAATTACAGGAGAAAAACGTGTGATGATCCTGAA 1696

RESULT 11

AA546124 standard; cDNA; 1515 BP.

AA546124;

18-DEC-2001 (first entry)

Human DNA encoding PRO polypeptide sequence #200.

PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
PCR primer.

Homo sapiens.

MO200168848-A2.

20-SEP-2001.

28-FEB-2001; 2001WO-US065520.

01-MAR-2000; 2000WO-US05601.
02-MAR-2000; 2000WO-US05841.
03-MAR-2000; 2000US-187202P.
06-MAR-2000; 2000US-186968P.
14-MAR-2000; 2000US-189320P.
14-MAR-2000; 2000US-189328P.
15-MAR-2000; 2000WO-US06884.
21-MAR-2000; 2000US-190828P.
21-MAR-2000; 2000US-191007P.
21-MAR-2000; 2000US-191048P.
21-MAR-2000; 2000US-191314P.
28-MAR-2000; 2000US-192655P.
29-MAR-2000; 2000US-193032P.
29-MAR-2000; 2000US-193053P.
30-MAR-2000; 2000WO-US08439.
04-APR-2000; 2000US-194449P.
04-APR-2000; 2000US-194647P.
11-APR-2000; 2000US-195975P.
11-APR-2000; 2000US-196000P.
11-APR-2000; 2000US-196187P.
11-APR-2000; 2000US-196690P.
11-APR-2000; 2000US-196820P.
18-APR-2000; 2000US-198121P.
18-APR-2000; 2000US-198585P.
25-APR-2000; 2000US-199397P.
25-APR-2000; 2000US-199550P.
25-APR-2000; 2000US-199654P.
03-MAY-2000; 2000US-201516P.
17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14841.
02-JUN-2000; 2000WO-US15264.
05-JUN-2000; 2000US-209832P.
28-JUL-2000; 2000WO-US20710.
22-AUG-2000; 2000US-0644848.
24-AUG-2000; 2000WO-US23328.
08-NOV-2000; 2000WO-US30952.
01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.

(GENTH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

DR MPI; 2001-602746/68.
DR P-PSDB; AAU29223.

PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -

PS Claim 2; Fig 399; 774p; English.

XX Sequences AA545925-AA546231 represent DNA molecules encoding and PCR
XX primers for PRO polypeptides of the invention. The sequences of the
XX invention can be used to detect the presence of a tumour in a mammal by
XX comparing the level of expression of a PRO polypeptide in a test sample
XX of cells from the animal and a control sample of normal cells, whereby a
XX higher level of expression in the test sample indicates the presence of a
XX tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
XX pigs, goats and rabbits but are preferably human. The polypeptides can be
XX used to stimulate tumour necrosis factor (TNF) alpha release from human
XX blood, when contacted with it. A specific polypeptide can be used to
XX stimulate the proliferation or differentiation of chondrocyte cells. The
XX CC PRO proteins can be used to determine the presence of tumours and also
XX CC susceptibility to tumour development, particularly adrenal, lung, colon,
XX breast, prostate, rectal, cervical, or liver tumours, in mammalian
XX subjects. The oligonucleotide probes specific for the PRO nucleic acids
XX can be used for genetic analysis of individuals with genetic disorders.

SQ Sequence 1515 BP; 404 A; 384 C; 363 G; 364 T; 0 other;

Query Match 49.1%; Score 963.6; DB 22; Length 1515;
Best Local Similarity 78.7%; Pred. No. 6; 8e-285;
Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;

QY 13 CGGGCCATGTTGCTAGTGTGCTGATCTTGCTGATCTGCTGAGAGAGCCCTGCTCGA 72
Db 1 CGGGCCATGTTGCTAGTGTGCTGATCTTGCTGATCTGCTGAGAGAGCCCTGCTCGA 60
QY 73 GAGCCGACTATTCAGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 132
Db 61 GAGCCGACTATTCAGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 133 ACACCTACTCCAG 192
Db 121 GATCTAATCCCGGAG 180
QY 193 GCAG 252
Db 181 ACAG 240
QY 253 CGCTTGTGAAGGCCACCAAGATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 312
Db 241 CGCTTGTGAAGGCCACCAAGATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 313 TGTGTGAG 372
Db 301 TGTGTGAG 360
QY 373 TGGACATCTCTGATGAG 432
Db 361 TGGACATCTCTGATGAG 420
QY 433 CATTAATCCCAATGCTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
Db 421 CATTAATCCCAATGCTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 493 TGGCCAG 552
Db 481 TCACCAAG 540
QY 553 CTGTGGAG 612
Db 541 CTGTGGAG 600
QY 613 ACAACCAATCCCTTGGAAACAGATACAGATTCTCATTCACAGGAGACGACATTGGGG 672

Sequence 1515 BP; 404 A; 384 C; 363 G; 364 T; 0 other;

Query Match 49.1%; Score 963.6; DB 22; Length 1515;
Best Local Similarity 78.7%; Pred. No. 6.8e-285;
Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;

QY 13 CGGGCCATGTTGCTAGAGTGTCTGATCTTGGCTCATGTCGAGAGAGCCCTGCTGCA 72
DB 1 CCGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
QY 73 GAGCGCATATTCAGTGTGCTGAGACAGGGCATCTCCAGAGTGGATGGTCCACAC 132
DB 61 GAGCGCATATTCAGTGTGCTGAGACAGGGCATCTCCAGAGTGGATGGTCCACAC 120
QY 133 ACATCTACTCCAGAGACTTGAAGGACCTCCAGTGAACCTCTCAAGACAGTGTGCA 192
DB 121 GATCTAATCCCGGAGCTTGAAGGACCTCCAGTGAACCTCTCAAGAGTGTGCA 180
QY 193 GCAGAGAGATTTCAATTTTATGACATTAAGCTGATCTCCGGGCAAGCCAGCATC 252
DB 181 ACAGGGGACTAATTCATTTGATGAATGTAAGTGGTACTCCGGGCAAGTCCAGCATC 240
QY 253 CGCTTTGTAAGGCGACCAAGATCTGGTGAAGGCAAAAACAATGAATTCATAGC 312
DB 241 CGCTTTGTAAGGCGACCAAGATTTGTTGAGCGGCAAAACATTCAGTCTTACAGC 300
QY 313 TGTGTAGTGTCACTACACAGAGGCTTCCAAAGCCAGACAGACCTTCCGGCGCAAA 372
DB 301 TGTGTAGTGTCACTACACAGAGGCTTCCAAAGCCAGACAGACCTTCCGGCGTAA 360
QY 373 TGAACATTTCTCTATGAGGCTTCCCTGTGAGCTGACACTCTCTATCTCATAGGCC 432
DB 361 TGAACATTTCTCTATGAGGCTTCCCTGTGAGCTGACAGCTGAACAGCTATTTGAGGCC 420
QY 433 CATTAACATCCCAATGCTAATATGATGAGACAGCCCTTCTTGTGTAAGTTCACC 492
DB 421 CATTAATTTCTCTAATGAAATATGAAATGAGATGGCCCTTCAATGTCTGAAATTTACC 480
QY 493 TCGCGAGGCTGCTTAAACCAAGTAAATATTAAGACAGTCACTGAGCGGGAAGC 552
DB 481 TCACGAGGCTGCTTAAACCAAGTAAATATTAAGACAGTCACTGAGCGGGAAGC 540
QY 553 CTGTGGGACCCAGACATCACTGCTTTGTAAGACAGAAAGATGTTGAAGTGAATTC 612
DB 541 CTGTGGGATCCGAACATCACTGCTTTGTAAGACAGAAAGATGAGAAAGTGAATTC 600
QY 613 ACAACCAATCCCTTGAAGACAGTACAGATCTCACTTAAGCGGACAGCACTTGGGG 672
DB 601 ACAACCAATCCCTTGAAGACAGTACAGATCTTAAATCCAAACAGCACTATATCGGG 660
QY 673 TTTTCTAGAGTGTG-----AGAAATAACTGATGAGAGCTGTAGCCATCCG 723
DB 661 TTTTCTAGAGTGTGAGCCACACAGAAAGAAACAAAGGAGTTGAGTGAATTTCCA 720
QY 724 GTGACTGAGAGAGTGAAGTGGGCTTCACTGACCTCAATTTTAACTACTGCGGC 783
DB 721 GTGACTGAGAGAGTGAAGTGGGCTTCACTGACCTCAATTTTAACTACTGCGGC 780
QY 784 AATGACTGATCCGACGCGAGGAGAGTGTGCTTGTCAAGAGACAATGCTCCCATC 843
DB 781 AGGACTGATCCGACATTAAGAGAGAGTGTGCTTGTCCCAACAAAGCGCTCCCTTC 840
QY 844 CTTCTCAGATGACAAACAGACCATGCTGGAGGCTGCTGCTCTCTTCTGTGAG-CTG 900
DB 841 CTTCTCAGATGACAAACAAAGAGAGGAGGCTGCTGCTCTCTCTGCTGTCTG 900
QY 901 CTGTGGCTGTGTGGTGTGCTGAGCTGAGTCTAATCTTGAAGGCAAGAGAGC 960
DB 901 CTGTGGCTGTGTGGTGTGCTGAGCTGAGTCTAATCTTGAAGGCAAGAGAGC 960
QY 961 AGAAGAGCTCTTCTCTATTTTCAACATGCTCTGCGCTCAATTAAGCTCTGAGGT 1020
DB 961 AAGAGAGCTCTCTCTCTA---CCACCACTACTGCCCCCATTAAGGTTCTTGTGTT 1017

QY 1021 TATCTTCTGAGATATGTTTTCATCAACCGTCTGCTTCACTGACTTTCTTCAAAAC 1080
DB 1018 TACCACTCTGAATATGTTTTCATCAACAAATTTGTTACTGCAATTTCTTCAAAAC 1077
QY 1081 TACTGCAAGAGTGAATGCTATCTTGAAGAAATGCAAGAAAGAAATGCCCGAGATGGG 1140
DB 1078 CATTTGCAAGAGTGAATGCTATCTTGAAGAAATGCAAGAAAGAAATGCAAGATGGG 1137
QY 1141 CCGTACAGTGTGCTGACCACTCAGAAAGAGCGGAGATTAAGTGTCTTCTTCTCC 1200
DB 1138 CCACTGCAAGTGTGCTGCACTCAAAAGAGGAGAGCAAGAAATGCTTCTTCTTCC 1197
QY 1201 AGTACGTCTCCGACCTTGTGACAGTCTGCTGCTGCAATAGAGGCAAGCGGAGAG 1260
DB 1198 AATGACGTCAACAGTGTGCGATGCTGCTGCTGCAAGAGGAGGAGTCCAGTGA 1257
QY 1261 AACTCTCAGATGTGTTCTTCTTCTGCTTTAACTTTTGTAGATTTTCAAGACCCAG 1320
DB 1258 AACTCTCAGATGTGTTCTTCTTCTGCTTTTAACTTTTGTAGATTTTCAAGACCCAG 1317
QY 1321 ACCATCTGCAAAATACCTGCTGCTTATCTTGGGGAGACAGACTCAAGGCACTAT 1380
DB 1318 ATTCATCTGCAAAATACCTGCTGCTTATCTTGGAGATTTATCAAAAGGCACTAT 1377
QY 1381 AATGCCCTGAGTGTGCTGCTTCCCAATATCATCTTATGAAGAGCGCACAGCTTTCCACACA 1440
DB 1378 AATGCTCTGAGTGTGCTGCTTCCCAAGTACCACTCATGAAGATGCCACTGCTTTCTGTGCA 1437
QY 1441 GAATCTTCAAGGCTACGAGAGCATGTCAGTGAAGAAACGCTCAACAGCTTCCATGAT 1500
DB 1438 GAATCTTCAAGGCTACGAGAGCATGTCAGTGAAGAAACGCTCAACAGCTTCCATGAT 1497
QY 1501 AGCTGTCAACCTTGTAG 1518
DB 1498 GGTCTGCTGCTCTTGTAG 1515

RESULT 13
AAE92136
ID AAE92136 standard; cDNA; 1515 BP.
XX
AC AAE92136;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PROS801 cDNA.
XX
KW Human; PRO protein; mapping; ss.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US23328.
XX
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 07-DEC-1999; 99US-0169495.
PR 09-DEC-1999; 99US-0170262.
PR 11-JAN-2000; 2000US-0175481.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 03-MAR-2000; 2000US-0187202.
PR 25-APR-2000; 2000US-0199397.
PR 22-MAY-2000; 2000WO-US14042.
PR 05-JUN-2000; 2000US-0209832.
XX
PA (GETH) GENENTECH INC.

KW cellular migration; ovulation; neurogenesis; arthritis;
 KW autoimmune disorder; systemic lupus erythromatosus; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 10..1290
 FT /tag= a
 FT /product= "interleukin 17-receptor-like protein"
 FT sig_peptide /tag= b
 FT mat_peptide 67..1287
 FT /tag= c
 PN WO200055204-A1.
 PD 21-SEP-2000.
 PF 06-MAR-2000; 2000MO-US05759.
 PR 16-MAR-1999; 99US-0268311.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Shi Y, Ruben SM;
 DR MPI; 2000-647065/62.
 DR P-PDB; AAB18750.
 XX
 PT Novel gene encoding a polypeptide of the interleukin-17 receptor family, and an antagonist and agonist of the polypeptide, useful for treating, diagnosing, detecting and/or preventing immune system related disorders
 PT
 PS Claim 2; Fig 1A-C; 247bp; English.
 CC The present sequence encodes a human interleukin 17-receptor-like protein (IL17R). The IL17R polypeptide is useful for screening for agonists and antagonists. These antagonists and agonists are useful for treating, diagnosing, detecting and/or preventing disorders related to cellular activation, haemostasis, angiogenesis, tumour metastasis, cellular migration, ovulation or neurogenesis, such as osteoporosis, arthritis and autoimmune disorders e.g. systemic lupus erythromatosus.
 CC
 SQ Sequence 1816 BP; 532 A; 439 C; 399 G; 445 T; 1 other;
 Query Match 49.1%; Score 963.6; DB 21; Length 1816;
 Best Local Similarity 77.4%; Pred. No. 7.6e-285;
 Matches 1236; Conservative 1; Mismatches 340; Indels 19; Gaps 5;

QY 373 TGGACATTCCTATGAGCTTCCTGAGAGCTGAGCACTCTATCTCATACAGCC 432
 DB 364 TGGACATTTTCTACATCGGCTTCCTGTAGAGCTGACACAGTCTATTTCAATGGGGCC 423
 QY 433 CATTAATCCCAATGCTATATGAATGAGACAGCCCTTTCTGTGTGAATCTTACC 492
 DB 424 CATTAATTCCTAATGCAATAATGAATGAAGAGCCCTTCAATGTCTGTGAATTTTACC 483
 QY 493 TCGCAGAGCTGCTTAACCAAGTATGAATATTAATAAGAGAGTCACTGAGGGGGAAGC 552
 DB 484 TCACAGAGCTGCTTAACCAAGTATGAATATTAATAAGAGAGTCACTGAGGGGGAAGC 543
 QY 553 CTGTGGACCCAGACATCATCTGCTTGAATAAAGAGAGAGAGTGAATGAATTTTC 612
 DB 544 CTGTGGAGTCCGAACATCACTGCTGTGAAGAAGAGAGAGACAGTGAAGTGAATTTTC 603
 QY 613 ACAACCAATCCCTTGGAAAAGATACAGATTTCTATTCACACGGGACACAGCATTTGGG 672
 DB 604 ACAACCAATCCCTTGGAAAAGATACAGATTTCTATCCACACAGCATATCATGTGGG 663
 QY 673 TTTTCTAGAGTGTGG-----AGAAATAACTGATGAGAGCTGTGAGCATCCG 723
 DB 664 TTTTCTAGAGTGTGG-----AGAAATAACTGATGAGAGCTGTGAGCATCCG 723
 QY 724 GTGACTGAGAGAGTGAAGTGGGTGCTTCACTGAGCCCATATTTATATATATATATAT 783
 DB 724 GTGACTGAGAGAGTGAAGTGGGTGCTTCACTGAGCCCATATATATATATATATATAT 783
 QY 784 AATGACTGATCCGACGCAAGGAGAGATTTGCTTGTCTACAGACAGATGTCTCCATC 843
 DB 784 AGGACTGATCCGACGCAAGGAGAGATTTGCTTGTCTACAGACAGATGTCTCCATC 843
 QY 844 CCTCCAGATGACAAACAGAGCATGTGGAGGCTGCTCTCTCTCTGAGG--CTG 900
 DB 844 CCTCCAGATGACAAACAGAGCATGTGGAGGCTGCTCTCTCTCTGAGG--CTG 900
 QY 901 CTGTGGCTGTGTGGGTGTGGAGCTGTGGATCTTAATCTTGAGAGCAAGAGAGAC 960
 DB 904 CTGTGGCTGTGTGGGTGTGGAGCTGTGGATCTTAATCTTGAGAGCAAGAGAGAC 963
 QY 961 AGCAAGACGCTCTTCTTCTATTTCCACAGTCTCTGCTCTATTAAGTCTCTGTGTT 1020
 DB 964 AAGCAAGACGCTCTTCTTCTATTTCCACAGTCTCTGCTCTATTAAGTCTCTGTGTT 1020
 QY 1021 TATCTTCTGAGATATGTTTCTCATACACGCTGTGCTGCTCATCTTCTTCAAAAC 1080
 DB 1021 TATCTTCTGAGATATGTTTCTCATACACGCTGTGCTGCTCATCTTCTTCAAAAC 1080
 QY 1081 TACTGCAAGAGTGAAGTCACTCTTGAATAAATGCGAGAGAGAGAGAGAGAGAG 1140
 DB 1081 TACTGCAAGAGTGAAGTCACTCTTGAATAAATGCGAGAGAGAGAGAGAGAGAGAG 1140
 QY 1141 CCGGTACAGTGTGACCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 DB 1141 CCGGTACAGTGTGACCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 QY 1201 AGTGAAGTCCCACTTGTGACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 DB 1201 AGTGAAGTCCCACTTGTGACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 QY 1261 AACTCTCAGAGTCTGTTCCCTCTTGTGCTTAACTCTTGTGTGATTTTACAGAGCCAG 1320
 DB 1261 AACTCTCAGAGTCTGTTCCCTCTTGTGCTTAACTCTTGTGTGATTTTACAGAGCCAG 1318
 QY 1321 ACGCATCTGCAAAATCTGCTGTGTATCTTTGGGAGAGAGAGAGAGAGAGAGAGAG 1380
 DB 1319 AATCATCTGCAAAATCTGCTGTGTATCTTTAGAGAGATTTGATCAAAAGAGAGAGAG 1378
 QY 1381 AATGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 DB 1379 AATGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1438

Oy	1441	GAACCTTCGAAAGGTAGCAGCAAGCATGTCAGTGAABAAAAGCGCCACAACCTGCATCAT	1500
Dd	1439	GAACTCTCTCCATGTCGAATGACAGGTGTCAAGCAGAAAAAAGATCACAAACCTGCCACAT	1498
Oy	1501	AGCGTTTCACCCTTGTAAGTCCACCCGGGGGAA--TAGAGACTCTGAAGCCTTCTACTCT	1558
Dd	1499	GGCTGCTGCTCTTGTATAGCCACCCCATGAAACCAAGWAGCCTTAAGGCTTCTATCCC	1556
Oy	1559	CCCTTCAGTGAACAATGCTGTGTGACGACTGTGAA	1594
Dd	1559	ACCAATTACAGGGAAAAAACGTGTGATGATCCTGAA	1594
<hr/>			
RESULT 15			
ID	AAZ52035	standard; cDNA; 1816 BP.	
XX	AAZ52035;		
AC	AAZ52035;		
XX			
DT	09-AUG-2000	(first entry)	
De	cDNA encoding interleukin 17-1-like receptor protein (IL17RLP)-1.		
XX			
Kw	Interleukin-17-1-like receptor protein; IL-17RLP; cytokine receptor;		
Kw	resistant chronic infection; acute infection; mycobacterial infection;		
Kw	T-cell proliferation; IL-2 biosynthesis; lymphocytic leukaemia;		
Kw	T-cell mediated autoimmune disease; hematopoiesis; sepsis; hybridoma;		
Kw	IL-6 expression; myeloma; plasmacytoma; Lemert's lymphoma;		
Kw	immunoprotective; cytostatic; hematopoietic; proliferative;		
Kw	antibacterial; ss.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	10..1290	
FT		/*tag= a	
FT		/product= "interleukin 17 like receptor protein"	
FT	sig_peptide	10..66	
FT		/*tag= b	
FT		/label= leader_sequence	
FT	sig_peptide	10..51	
FT		/*tag= c	
FT		/label= leader_sequence	
FT		/note= "This corresponds to an alternative leader peptide as described on page 3 of the specification"	
FT	mat_peptide	67..1287	
FT		/*tag= d	
FT		/product= "Mature IL17RLP"	
FT	mat_peptide	52..1287	
FT		/*tag= e	
FT		/product= "Mature IL17RLP"	
FT		/note= "this is an alternative mature protein as described on page 3 of the specification"	
XX			
PN	WO200015759-A1.		
XX			
PD	23-MAR-2000.		
XX			
PF	15-SEP-1999;	99MO-US21048.	
XX			
PR	16-SEP-1998;	98US-0154219.	
XX			
PR	16-SEP-1998;	98MO-US19121.	
XX			
PR	16-MAR-1999;	99US-0268311.	
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX			
Pi	Ruben SM, Shi Y;		
XX			
DR	WPI: 2000-271403/23.		
XX			
DR	P-PsDB; AAY70591.		
XX			
PT	Novel polynucleotides encoding interleukin-17-1-like receptor protein,		
XX	useful for diagnosis and treatment of immune system-related disorders,		
XX			

PT	e.g. sepsis and cancers -
XX	Claim 2; Fig 1; 147pp; English.
PS	The patent relates to novel interleukin-17-like receptor
CC	protein (IL-17R _p). IL-17R _p is a homologue of the IL-17 receptor and has
CC	a wide range of cytokine receptor-like activities. IL-17R _p or its
CC	agonists may be used to enhance host defenses against resistant chronic,
CC	and acute infections, e.g. mycobacterial infections, via the attraction
CC	and activation of microbicidal leukocytes. It may also be used to
CC	increase T-cell proliferation by stimulating IL-2 biosynthesis, for the
CC	treatment of T-cell mediated autoimmune diseases and lymphocytic
CC	leukemia. IL-17R _p may also be used to regulate hematopoiesis and to
CC	treat sepsis. Extracellular IL-17R _p domains may be used as antagonists
CC	of IL-17R _p . IL-17R _p agonists and antagonists can also be used to
CC	modulate IL-6 expression, useful in treatment of cancers such as
CC	myelomas, plasmacytomas and hybridomas and Lemmer's lymphoma. The
CC	present cDNA sequence encodes human IL-17R _p . This cDNA sequence was
CC	discovered in a cDNA library derived from human adult pulmonary tissue.
XX	
SQ	Sequence 1816 BP; 532 A; 439 C; 399 G; 445 T; 1 other;
	Query March 49.1%; Score 963.6; DB 21; Length 1816;
	Best Local Similarity 77.4%; Pred. No.7.6e-285;
	Matches 1236; Conservative 1; Mismatches 340; Indels 19; Gaps 5
OY	13 CGGGCACTGTTGTAGTATGTCGATCTTGCGCATGTCGACGAGCGCCCTGCCTCGA 72
DB	4 CGAGGAGTGTGGCTGTCTCTGTAAGCCTGGCGCGCTGTGACGAGACGCCGTACCCGA 63
OY	73 GAGCCGACTATTCAAGTGTGCTCTGAGACAGGCGCATCTCCAGAGTGGTCCAACAC 132
DB	64 GAGCGGACCGTTCAATGTCGCTTGAACTGGGCGCATCTCCAGAGTGGTCTAACACAT 123
OY	133 AACACTCACTCCAGAGACTTAGAGGAGACCTCCAGTGGAACTGTGCAAGCAAGTGGGA 192
DB	124 GATCTAAATCCCCGAGACTTAGAGGACCTCCGAGTAGAACCTGTTCACAATAAGTGTGA 183
OY	193 GCAGAGAGGTTTCAATTTATGTAACATAAGCTGATGTAATCCGGCGAGACCAGCATC 252
DB	184 ACAAGGAGCATATCAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 243
OY	253 CGCTTGTGAAGGCCACCAAGAATCTGCGTGAAGTGGCAAAAACAATGATTCATPACAC 312
DB	244 CGCTTGTGAAGGCCACCAAGAATTTGTGTGACGGGCAAAAGCACTTCCAGTCTACACG 303
OY	313 TTGTGTAGAGTGCATACACAGAGGCTTCCAAAGCCAGACCAACCTTCGGGGCGCAA 372
DB	304 TTGTGTAGAGTGCATATCACAGAGGCTTCCAGATCCAGACCAACCTTCGTGTGTAA 363
OY	373 TGGAATCTCTCTAATGTATGAGGCTCCCTGTGAGAGTGCAGACCTCTATCTCATACGGCC 432
DB	364 TGGAATCTCTCTAATGTATGAGGCTCCCTGTGAGAGTGCAGACCTCTATCTCATACGGCC 423
OY	433 CATACATCCCCCAATGTCTAATATGATGAGACAGCCCTTCTTTGTCTGTGAATCTCAC 492
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 22:37:09 ; Search time 4999.22 Seconds

(without alignments)
11427.544 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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6	988.2	50.3	1841	6	AX253204
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8	985.8	50.2	2042	9	BC000980
9	983	50.1	1796	6	AX350967
10	980.8	50.0	1828	9	AF208110
11	971.2	49.5	1583	9	AF250309
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ALIGNMENTS

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VERSION AF208108.1 GI:9246428
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1963)
REFERENCE Tian, E., Sawyer, J.R., Largaespada, D.A., Jenkins, N.A., Copeland, N.G.
and Shaughnessy, J.D., Jr.
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TITLE Evi27 encodes a novel membrane protein with homology to the IL17 receptor
 JOURNAL Oncogene 19 (17), 2098-2109 (2000)
 MEDLINE 20273223
 PUBMED 10815801
 REFERENCE 2 (bases 1 to 1963)
 AUTHORS Snaughnessy, J.D., Jr.
 TITLE Direct Submission
 JOURNAL Submitted (24-NOV-1999) Myeloma and Transplantation Research Center, University of Arkansas for Medical Sciences, 4301 W. Markham St, Little Rock, AR 72212, USA

FEATURES

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REFERENCE 1 (bases 1 to 2018)

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AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (02-Apr-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcdpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

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through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
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VERSION AF208109.1 GI:9246430
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 (bases 1 to 2589)
Tian, E., Sawyer, J.R., Largaespada, D.A., Jenkins, N.A., Copeland, N.G.
and Shaughnessy, J.D., Jr.
Evl27 encodes a novel membrane protein with homology to the IL17
receptor
JOURNAL Oncogene 19 (17), 2098-2109 (2000)
MEDLINE 20273223
PUBMED 10815801
2 (bases 1 to 2589)
Shaughnessy, J.D., Jr.
Direct Submission
AUTHORS Submitted (24-NOV-1999) Myeloma and Transplantation Research
Center, University of Arkansas for Medical Sciences, 4301 W.
Markham St, Little Rock, AR 72212, USA
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RESULT 4
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AC093357.1 GI:15213902
HTG, HTGS_PHASE1, HTGS_DRAFT, HTGS_FULLTOP.
SOURCE Mus musculus.
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Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 234131)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Unpublished
2 (bases 1 to 234131)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
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Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT
Submitted (20-AUG-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Genome Center
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L13729
Center clone name: 25 A 7
Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
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Consensus quality: 225885 bases at least Q40
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Insert size: 232831; sum-of-contents
Quality coverage: 10.4 in Q20 bases; agarose-efp
Quality coverage: 9.4 in Q20 bases; sum-of-contents

* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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2106 2205: gap of 100 bp
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DEFINITION Sequence 56 from Patent WO0149728.
ACCESSION AX191534
VERSION AX191534.1 GI:15209722
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1818)
AUTHORS Kato, S. and Kimura, T.
TITLE Human proteins having hydrophobic domains and dnas encoding these
proteins
JOURNAL Patent: WO 0149728-A 56 12-JUL-2001;
Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)
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RESULT 7
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LOCUS Sequence 17 from Patent WO208285.
DEFINITION AX365258
ACCESSION AX365258
VERSION AX365258.1 GI:18697003
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Medlock, E., Yeh, R., Silbiger, S.M., Elliott, G.S., Nguyen, H.Q. and
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Patent: WO 0208285-A 17 31-JAN-2002;
JOURNAL
Amgen, Inc. (US)
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BASE COUNT 522 a 455 c 416 g 448 t
ORIGIN

Query Match 50.3%; Score 988.2; DB 6; Length 1841;
Best Local Similarity 77.9%; Pred. No. 2.3e-287;
Matches 1248; Conservative 0; Mismatches 338; Indels 17; Gaps 4;

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Qy	777	CTGCGGCAATGACTGCATCCGACCGCAGAGGGAACAGTTGTCTTTGCTCAGACAAAGTGC	836
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Qy	837	TCCCATCCCTCCAATGACACACAGCGATGCTGGAGAGTGGGTCTCTCTCTGTGT	896
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LOCUS	BC000980	2042 bp	mRNA	linear	PRI 12-JUL-93
DEFINITION	Homo sapiens, clone MGC:5245 IMAGE:2985728, mRNA, complete cds.				
DESCRIPTION	MGC:5245 IMAGE:2985728				

KEYWORDS MGC.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS
Strausberg, R.

Gene Collection (MGC), Cancer Genomics Office, National Cancer

REMARK
NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Tissue Procurement: ATCC

DNA Sequencing by: Baylor College of Medicine Human Genome

Center code: BCM-HSCC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,

Clone distribution: MGC clone distribution information can be found

This clone was selected for full length sequencing because it

FEATURES
SOURCE

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BASE COUNT 625 a 484 c 426 g 507 t
ORIGIN

Query Match 50.2%; Score 985.8; DB 9; Length 2042;
Best Local Similarity 77.9%; Pred. No. 1.2e-286;
Matches 1245; Conservative 0; Mismatches 337; Indels 17; Gaps 4;

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DEFINITION Sequence 1 from Patent WO0190358.
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VERSION AX350967.1 GI:18616343
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unclassified.
unclassified.
REFERENCE
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AUTHORS Gorman,D.M.
TITLE Mammalian receptor proteins; related reagents and methods
JOURNALS Patent: WO 0190358-A 1 29-NOV-2001;
SCHERING CORPORATION (US)
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ORIGIN

Query Match 50.1%; Score 983; DB 6; Length 1796;
 Best local Similarity 77.9%; Pred. No. 8,6e-286;
 Matches 1241; Conservative 0; Mismatches 335; Indels 17; Gaps 4;

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RESULT 10
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 LOCUS AF208110
 DEFINITION Homo sapiens IL-17 receptor homolog precursor (EVI27) mRNA,
 complete cds.
 ACCESSION AF208110
 VERSION AF208110.1 GI:9246432
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 Tian, E., Sawyer, J.R., Largaespada, D.A., Jenkins, N.A., Copeland, N.G.
 and Shaughnessy, J.D., Jr.
 EVI27 encodes a novel membrane protein with homology to the IL17
 receptor
 JOURNAL Oncogene 19 (17), 2098-2109 (2000)
 MEDLINE 20273223
 PUBMED 10815801
 REFERENCE 2 (bases 1 to 1828)
 AUTHORS Shaughnessy, J.D., Jr.
 TITLE Direct Submission
 JOURNAL Submitted (24-NOV-1999) Myeloma and Transplantation Research

Center, University of Arkansas for Medical Sciences, 4301 W.
 Markham St., Little Rock, AR 72212, USA

FEATURES

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 Best Local Similarity 77.8%; Pred. No. 46-285;
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RESULT 11
 AF250309 1583 bp mRNA linear PRI 17-APR-2001

LOCUS AF250309 Homo sapiens putative cytokine receptor CRL4 precursor mRNA,
 DEFINITION complete cds.

ACCESSION AF250309 GI:13649476

VERSION AF250309.1
 KEYWORDS Homo sapiens.
 SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1583)
 AUTHORS Zhang, W. and Cao, X.
 TITLE Direct Submission
 JOURNAL Submitted (29-MAR-2000) Department of Immunology, Second Military
 Medical University & Shanghai Brilliance Biotechnology Institute,
 800 Xiangyin Rd., Shanghai 200433, P.R. China

FEATURES
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BASE COUNT 427 a 397 c 377 g 382 t

Query Match 49.5%; Score 971.2; DB 9; Length 1583;
 Best Local Similarity 78.6%; Prid. No. 3.2e-282;
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LOCUS AX092426 1515 bp DNA linear PAT 23-MAR-2001
 DEFINITION Sequence 157 from Patent WO0116318.
 ACCESSION AX092426
 VERSION AX092426.1 GI:13444527
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1515)
 Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
 Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
 Wood,M.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same

JOURNAL Patent: WO 0116318-A 157 08-MAR-2001;
 Genentech, Inc. (US)

FEATURES Location/Qualifiers
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source
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 Best Local Similarity 78.7%; Pred. No. 6,3e-280;
 Matches 1194; Conservative 0; Mismatches 309; Indels 15; Gaps 3;
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 Db 1 CCGGCCATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
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 Db 121 GATCTAATCCCGGAGACTTGAAGAGCTTCCAGAGTGAACCTGTCAAAGCAAGTGTGGA 180
 QY 193 GCAGAGAGTTCATATTTGATGAACATATGATGATGATGATGATGATGATGATGATGATG 252
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Qy 1501 AGCTGTTCAACCCCTGTAG 1518
Db 1498 GGCTGCTGCTCTTGTAG 1515
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Job time : 5282.72 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 23:21:54 ; Search time 3594.88 Seconds

(without alignments)
11663.832 Million cell updates/sec

Title: US-09-778-971-4

Perfect score: 2589
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	624	24.1	678	10	BB307800
3	502.4	19.4	646	10	BB644125
4	489.4	18.9	773	13	BB103740
5	488.4	18.9	710	10	BB653710
6	439	17.0	439	9	AA144114

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9	366.8	14.2	370	9	AA562342	AA562342	
10	366	14.1	652	14	BM693867	BM693867	
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15	352	13.6	588	13	B1360842	B1360842	
16	349.2	13.5	946	13	B1823321	B1823321	
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18	333.2	12.9	676	10	AV727345	AV727345	
19	330.2	12.8	680	10	AM970151	AM970151	
20	313.2	12.1	572	13	BM030860	BM030860	
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ALIGNMENTS

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LOCUS BB667509 728 bp mRNA linear EST 24-OCT-2001
DEFINITION BB667509 RIKEN full-length enriched, adult male liver tumor Mus
ACCESSION BB667509
VERSION BB667509.1 GI:16398958
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 728)
AUTHORS Arakawa,T., Carinci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,U., Komoto,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okio,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saito-cho, Tsukuba, Ibaraki, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
 M., Komono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. *Genome Res.* 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
 Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multichannel sequencer. *Genome Res.*
 10 (11), 1757-1771 (2000)
 Komono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
 Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
 Komono, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
 K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 e mouse tissues.

FEATURES

Location/Qualifiers
 1. 728
 /organism="Mus musculus"
 /db_xref="taxon:10090"
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 tumor"
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 /lab_host="DH10B"
 /note="Site 1: Sali; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5']
 GAGAGAGAGAGCGCGCGCACTCGAGTTTCTTTTCTTTTNN 3']. cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence [5']
 GAGAGAGAGATCTCGAGTTTAATTAATTAATATCCCCCCCC 3']. cDNA
 was cleaved with BamHI and XhoI. Vector: a modified
 Bluescript KS(+) after bulk excision from Lambda FIC I.
 Tissue was provided by William A. Held, Roswell Park
 Cancer Institute, Department of Molecular and Cellular
 Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose
 assistance we gratefully acknowledge."

BASE COUNT 189 a 180 c 167 g 188 t 4 others

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 Best Local Similarity 97.5%; Pred. No. 2e-117;
 Matches 658; Conservative 0; Mismatches 14; Indels 3; Gaps 2;

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 DB 2019 GTCTGCCCAATATATCATCATGAAGAGAGAGCTTTCCACAGAACTTCTCAAG 2078

DB 119 GTTGGCCCCCAATATATCATCTCATGAAGAGAGCGCCAGAGCTTTCCACAGAACTTCTCAAG 178
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RESULT 2
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 ACCESSION BB307800.2 GI:15411368
 VERSION
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 678)
 ARAKAWA, T., CARNINCI, P., FUKUDA, S., FURUNO, M., HANAGAKI, T., HARA, A.,
 HIRAMOTO, K., HORI, F., ISHII, Y., ITO, M., KAWAI, J., KOMONO, H., KOUNDA
 M., KOYA, S., MATSUYAMA, T., MIYAZAKI, A., NOMURA, K., OHNO, M.,
 OKAZAKI, Y., OKIDO, T., SAITO, R., SAKAI, C., SAKAI, K., SANO, H., SASAKI
 D., SHIBATA, K., SHINAGAWA, A., TAKAHASHI, F., TAKEDA, Y., TANAKA, T., TOYA, T.,
 TAGAMI, M., TAGAWA, A., TAKAHASHI, F., TAKEDA, Y., TANAKA, T., TOYA, T.,
 MURAMATSU, M. and HAYASHIZAKI, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished (2001)
 On Jul 10, 2000 this sequence version replaced gi:9008505.
 CONTACT: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel.: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh

Position	Sequence	Position
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DEFINITION	AA144114				
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	5', mRNA sequence.				
ACCESSION	AA144114				
VERSION	AA144114.1	GI:1713482			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				

REFERENCE 1 (bases 1 to 439)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gessel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thaisang,B., Wylie,T., Lennon,G., Soares,B., Wilson,R.,
Maerstrom,R.
TITLE The Mashu-HMMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project

TITLE The Mashu-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
 Washu-HHMI Mouse EST Project
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LINL, the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:358377
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 430.

FEATURES	Location/Qualifiers
source	1. .439

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was primed with a Not I - oligo(dT) primer [5',
TGTTCACCAATCTGAAGTGGGACGGCGCTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M. Fatima Bonaldo."

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BASE COUNT	91 a	120 c	98 g	130 t
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Best Local Similarity 100.0%; Pred. No. 7.6e-79;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	801	TTGTTGTGAGGCTGTGC	819
Db	421	TTGTTGTGAGGCTGTGC	439

RESULT 1	BF322373/c	431 bp	mRNA	linear	EST 21-NOV-2000
LOCUS	ma224807.x1	NCI_CGAP_L110	Mus musculus	CDNA clone	IMAGE:3811861 3'
DEFINITION	mRNA sequence.				
ACCESSION	BF322373				
VERSION	BF322373.1				
KEYWORDS	GI:11271749				
SOURCE	EST.				
ORGANISM	house mouse.				
	Mus musculus				

REFERENCE 1 (pages 1 to 431)
AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

Email: CGAD@lml.nhlbi.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>

MG1:1453973
Seq primer: -40UP from Gibco
High quality sequence stop: 367.
location/Qualifiers
1. .431
source

```

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3811861"
/clone_1ib="NCI_CGAP_L110"
/sex="Female"
/dev_stage="10 weeks"
/lab_host="DH10b (r1 phage-resistant)"
/note="Organ liver; Vector: pCMV-SORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

```

Average insert size 1.6 kb. Library constructed by Life Technologies."

BASE COUNT 104 a 108 c 119 g 100 t
 ORIGIN
 Query Match 16.6%; Score 431; DB 12; Length 431;
 Best Local Similarity 100.0%; Pred. No. 3.2e-77;
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1822 TTCACGATGACCTCCGACCTTTTGACAGTCCGTGGCCAAATGAGGCGAGCCCA 1881
 431 TTCCAGATGACCTCCGACCTTTTGACAGTCCGTGGCCAAATGAGGCGAGCCCA 372
 1882 GGGAGAACTCTCAGATCTGTTCCCTTTGACCTTTTAACTTTTGTAGTGAATTCAGCA 1941
 371 GGGAGAACTCTCAGATCTGTTCCCTTTGACCTTTTAACTTTTGTAGTGAATTCAGCA 312
 1942 GCGAAGCATCTGACCAAAATACCTGCTGTATTTTGGGAGACAGACTCAAAAGGCG 2001
 311 GCGAAGCATCTGACCAAAATACCTGCTGTATTTTGGGAGACAGACTCAAAAGGCG 252
 2002 ACTATATATCCCTGAGTGTCTGCCCAATATCATCTCATGAGGACGCGACAGCTTTCC 2061
 251 ACTATATATCCCTGAGTGTCTGCCCAATATCATCTCATGAGGACGCGACAGCTTTCC 192
 2062 ACACAGAACTTTCTCAAGGCTACGACAGAGCATGTCACTGAAGAAAGCGCTCAAGCTTCC 2121
 191 ACACAGAACTTTCTCAAGGCTACGACAGAGCATGTCACTGAAGAAAGCGCTCAAGCTTCC 132
 2122 ATGATAGCTGTTCACCTTGTAGTCCACCGGGGGAATGAGACTCTGAAGCTTCTTAC 2181
 131 ATGATAGCTGTTCACCTTGTAGTCCACCGGGGGAATGAGACTCTGAAGCTTCTTAC 72
 2182 TCTCCCTTCAGTGAACAAATGCTGTGTGACGACTCTGAAGTGTGGGAGAGGCTGTG 2241
 71 TCTCCCTTCAGTGAACAAATGCTGTGTGACGACTCTGAAGTGTGGGAGAGGCTGTG 12
 2242 GAGTAGTGTCT 2252
 11 GAGTAGTGTCT 1

RESULT 8
 LOCUS A1158709 425 bp mRNA linear EST 30-SEP-1998
 DEFINITION U010d07.r1 Soares thymus_2NBMT Mus musculus cDNA clone
 IMAGE:1345453 5', mRNA sequence.
 ACCESSION A1158709
 VERSION A1158709.1 GI:3687178
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 425)
 Author(s) Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R., and
 Waterston, R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MG1:694245
 Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 402.
 Location/Qualifiers

FEATURES
 source
 1..425
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:1345453"
 /clone_1id="Soares_thymus_2NBMT"
 /sex="male"
 /tissue type="Thymus"
 /dev stage="4 weeks"
 /lab_host="DH10B"
 /note="Vector: p773D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGCGCGGCTTTTATTTTATTTTATTTT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified p773 vector. RNA
 provided by Dr. Bertrand Jordan. Library went through two
 rounds of normalization, and was constructed by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT 117 a 107 c 103 g 98 t
 ORIGIN

Query Match 16.4%; Score 423.4; DB 9; Length 425;
 Best Local Similarity 99.8%; Pred. No. 1.1e-75;
 Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1932 GATTTTCAGAGCGCAACGATCTGCACAAAATACCTGAGTGTCTATCTTGGGGAGAGAC 1991
 1 GATTTTCAGAGCGCAACGATCTGCACAAAATACCTGAGTGTCTATCTTGGGGAGAGAC 60
 1992 CTCAAAGGAGACTAATATGCTGAGTGTCTGCCCAATATCATCTCATGAAAGAGCC 2051
 61 CTCAAAGGAGACTAATATGCTGAGTGTCTGCCCAATATCATCTCATGAAAGAGCC 120
 2052 ACAGCTTTCCACACAGAACTTCTCAAGGCTACGACAGAGATGTCAAGAAAGCTTCA 2111
 121 ACAGCTTTCCACACAGAACTTCTCAAGGCTACGACAGAGATGTCAAGAAAGCTTCA 180
 2112 CAAGCTGCGATGATGCTGTTCACCTTTGTAGTCCACCGGGGGAATGAGACTCTGAA 2171
 181 CAAGCTGCGATGATGCTGTTCACCTTTGTAGTCCACCGGGGGAATGAGACTCTGAA 240
 2172 GCTTCCCTACTCTCCCTCCAGTGAACAAATGCTGTGACGACTCTGAAATGTGGGAG 2231
 241 GCTTCCCTACTCTCCCTCCAGTGAACAAATGCTGTGACGACTCTGAAATGTGGGAG 300
 2232 AGGCTGTGAGAGTAGTGTATGTAACAACCTTGCTTAAACTGGAAGTTGCAAGTCA 2291
 301 AGGCTGTGAGAGTAGTGTATGTAACAACCTTGCTTAAACTGGAAGTTGCAAGTCA 360
 2292 ACCTGAGCATACACCGCTGAGGCTTGTCAATGCTGGAATTTATGAACACACAGCTTAC 2351
 361 ACCTGAGCATACACCGCTGAGGCTTGTCAATGCTGGAATTTATGAACACACAGCTTAC 420
 2352 AGACA 2356
 421 AGACA 425

RESULT 9
 LOCUS AA562342 370 bp mRNA linear EST 18-AUG-1997
 DEFINITION V122h03.r1 StrataGene mouse Tcell 937311 Mus musculus cDNA clone
 IMAGE:973013 5', mRNA sequence.
 ACCESSION AA562342
 VERSION AA562342.1 GI:2333807
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 370)
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE The Washu-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 Washu-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:553741
 Putative full length read
 Vector to vector length is 377
 Seg primer: -28m13 rev1 ET from Amersham
 High quality sequence stop: 326.
 Location/Qualifiers

FEATURES

source

1. 370
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:973013"
 /clone_1ib="Stratagene mouse Tcell 937311"
 /tissue_type="Tcell"
 /dev_stage="M30 CD4+ cells"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: blood; Vector: pBluescript SK-; Site 1:
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
 Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGCAG
 3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."
 BASE COUNT 105 a 73 c 91 g 101 t
 ORIGIN

Query Match 14.2%; Score 366.8; DB 9; Length 370;
 Best Local Similarity 99.5%; Pred. No. 3.4e-64;
 Matches 358; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2212 GACTGCAATGTTGTGGAGAGGCTGTGTGAGGTAGTCTATGTAACAACCTTGCTTAA 2271
 1 GACTGCAATGTTGTGGAGAGGCTGTGTGAGGTAGTCTATGTAACAACCTTGCTTAA 60
 2272 AACTGAGTTTGCAGAGTCACTGAGCATACACGCTGAGGCTAGTCATTGCTGATT 2331
 61 AACTGAGTTTGCAGAGTCACTGAGCATACACGCTGAGGCTAGTCATTGCTGATT 120
 2332 TAAGAAGACACACAGTTATACATATATGATGGAGCACTTATGGAATATACCCAA 2391
 121 TAAGAAGACACACAGTTATACATATATGATGGAGCACTTATGGAATATACCCAA 180
 2392 AGCTGGATATGATTAATCACTGAGAACCCAGCACTCGGCCATGAGTAATACGCACTT 2451
 181 AGCTGGATATGATTAATCACTGAGAACCCAGCACTCGGCCATGAGTAATACGCACTT 240
 2452 CCTGTGAGGCTGTGTGAGGTTGCTGTGTGAGCACTGCCATGCTTATAGTGCAC 2511
 241 CCTGTGAGGCTGTGTGAGGTTGCTGTGTGAGCACTGCCATGCTTATAGTGCAC 300
 2512 GTAGACCGTTTGTATACATTTATCTGTTAATGAAATATCGTTGGGAAGCTTCAAA 2571
 301 GTAGACCGTTTGTATACATTTATCTGTTAATGAAATATCGTTGGGAAGCTTCAAA 360
 2572 AAAAAAAAAA 2581
 361 AAAAAAAAAA 370

RESULT 10
 LOCUS BM693867 652 bp mRNA linear EST 26-FEB-2002
 DEFINITION UI-E-DWI-ane-1-22-0-UI.r1 UI-E-DWI Homo sapiens cDNA clone
 accession
 VERSION BM693867.1 GI:19007125
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 652)
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 genome Res. 6 (9), 791-806 (1996)
 JOURNAL
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M3 Reverse.

FEATURES

source

1. 652
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-E-DWI-ane-1-22-0-UI"
 /clone_1ib="UI-E-DWI"
 /tissue_type="lens"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pRT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-E-DWI is a normalized cDNA library containing the
 following tissue(s): lens. The library was constructed
 according to Bonaldi, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pRT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CGATTAGCGA. This library
 was created for the program, Gene Discovery in the Visual
 System, supported by National Eye Institute (NEI)."
 BASE COUNT 188 a 167 c 135 g 162 t
 ORIGIN

Query Match 14.1%; Score 366; DB 14; Length 652;
 Best Local Similarity 76.0%; Pred. No. 4.2e-64;
 Matches 465; Conservative 0; Mismatches 145; Indels 2; Gaps 1;

1591 AAGAGCTCTTTCCTATTCACCAATGCTTCGCTTATTAAGTCTGCTGCTTATC 1650
 1 AAGAGCTCTTTCCTATTCACCAATGCTTCGCTTATTAAGTCTGCTGCTTATC 60
 1651 CTTCGAGATATGTTTCATCACACCGTGTGCGTTACGAGCTTCTTCAAACTACT 1710
 61 CATTGCAATATGTTTCATCACACCGTGTGCGTTACGAGCTTCTTCAAACTACT 120
 1711 GCAGAGTGAAGTCACTCTTGAATAATGCGAGAAAAATATCCGAGATGGGCGCG 1770

RESULT 11	LOCUS	DEFINITION
AI616016	AI616016	518 bp mRNA linear EST 21-APR-1999 mg66h01.v1 Soares thymus_2nbwt Mus musculus CDNA clone IMAGE:5837299 5', mRNA sequence.

```

FEATURES
source
location/Qualifiers
1..518
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:583729"
/clone_lib="Soares_thymus_2NbWT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DHI08"
/note="Vector: pT73D-Pac (Pharmacia) with a modified

```

Query Match	13.9%	Score 360;	DB 9;	Length 518;
Best Local Similarity	96.8%	Pred. No. 7	4e-63;	
Matches 420;	Conservative	0;	Mismatches 7;	Indels 7;
				Gaps 5;

AL565993/c	908 bp	mRNA	linear	EST 16-FEB-2001
LOCUS	AL565993			
DEFINITION	AL565993 LTI FL013 FBrn1 Homo sapiens CDNA clone CS0DF016YG03 3 prime, mRNA sequence.			

ACCESSION	AL565993
VERSION	AL565993.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayres, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES	Location/Qualifiers
SOURCE	1..908
	/organism="Homo sapiens"
	/db_xref="taxon:9606"

BASE COUNT
ORIGIN

225 a 172 c 223 g 259 t 29 others

```
/clone="CSODP016YG03"  
/clone_1ib="Ltr Fl013 Fbrn1"  
/dev_sfile="pooled tissue from post conception fetuses (20  
week, 24 week and 26 week)"  
/lab_host="DH10B"  
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand  
cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-stranded cDNA was digested with Not I  
and cloned into the Not I and Eco RV sites of the  
pCMVSPORT 6 vector. Library was constructed by Life  
Technologies. Contact : Feng Liang Life Technologies, a  
division of Invitrogen 9800 Medical Center Drive Rockville  
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :  
fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"
```

Query Match	13.8%	Score 357.4	DB 9	Length 908
Best Local Similarity	70.4%	Pred. No. 2.1e-62		
Matches 544; Conservative	22	Mismatches 195	Indels 12	Gaps 7

[illegible][illegible]

REFERENCE
1 (bases 1 to 551)
Fahrenkrug, S. C., Fekking, B. A., Rohrer, G. A., Smith, T. P. L., Casaa, E.,
AUTORS

TITLE	Design and use of two pooled tissue normalized cDNA libraries for
JOURNAL	EST discovery in swine
COMMENT	Unpublished (2000)
	Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel.: 402 762 4366
Fax: 402 762 4390
Email: emilt@mail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.960904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

FOR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 91 row: J column: 1
Seq primer: ATTTAGTGCACTATAG.

FEATURES	Location/Qualifiers
source	1. .551

```

/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

```

Query Match	13.7%	Score 353.6	DB 12	Length 551
Best Local Similarity	81.3%	Pred. No. 1.4e-61		
Matches 410, Conservative	0	Mismatches 94	Indels 0	Gaps 0

QY	1	GTGACCAGTGGCGGGG	CATGTTGCTAGTGTGTGATCTTGGCTGCAATGTCAGAGC	60	
Db	9	GGGGAAAGTGGCCCC	GGATGTTACTGATCTGAGCCTGGCCGCTGTGTGGGGT	68	
QY	61	GCCCTGCTCGAAGCCG	ACTATTCAGTGTGGCTCTGAGA	CAGGGCCATCTCCAGAGTGG 120	
Db	69	GCCATGCTTCCAGAGCCG	CAATTCAAGTGTGGCTCTGAGCCTGGA	CTGTCTCCAGAAATGG 128	
QY	121	ATGTCGCAACACACTC	ACTCCAGAGACTTGAAGGACCTCCAA	ATGGAACTGCTCAAG 180	
Db	129	ATGATTCGACACCTCTG	ACCCGAGAGACTTGAAGGACCTCCGAGTGA	AACTTATTTAAA 188	
QY	181	ACAAGTGTGGCACA	CAGAGAGTTTCAATTTTATGAA	CACTAAGCTGGATCTCCGGCA 240	
Db	189	AGCAGTGTGCATGAG	AGACTTATTTTATGAACTAAGCTGTG	ATCTCCGGCA 248	
QY	241	GACGCCAGCATCCGCT	TTGTTGAAGGCCACCAAGATCTGCGT	AGTGGCAAAAA	CAACATG 300
Db	249	GATGCCAGTATCCGAT	TTGTTGAAGGCCACCAAGATCTGTGTG	ACGGGCAAGACCCAAAG 308	
QY	301	AATTCATTACGCTGT	GTGTGAGTGCACTACACAGAGGCTTCCAA	AGCCAGACCAACCT 360	

DB	309	CAGACCTACAGCTGGGTGAGCGCAATTACATGAGAGCGCTTCACACTGACACGAGACT	368
OY	361	TCGGCGGCAATGATGACATCTTCCTATGTAGCGCTTCCTGTGAGCTGACACTCTAT	420
DB	369	TCGTGGCGGCAATGATGATGTTTCTCACTGAGCGCTTCCTGAGCTGCAATACAGCTAT	428
OY	421	CTCATCAGCGCCCATTAACATCCCAATGCTATATGAATGAGACAGCCCTCTTGTCT	480
DB	429	TTTCATTGAGCCCATTAATATCCCAATGCAATATGACGAAGAGGCGCCCTCTTGTGCT	488
OY	481	GTGAATCTACCTCGCAGGCTGC	504
DB	489	GTGAATCTACCTCGCAGGCTGC	512
RESULT 14			
LOCUS	BB284760	523 bp	mRNA
DEFINITION	BB284760	RIKEN full-length enriched, adult retina	mus musculus cDNA
ACCESSION	BB284760		
VERSION	BB284760.1	GI:8985209	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
AUTHORS	Komo, H., Akawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koyama, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Sugihara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamana, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.		
TITLE	RIKEN Mouse ESTs (Komo, H., et al.)		
JOURNAL	unpublished (2000)		
COMMENT	Contact: Yoshinide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/ Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S., Sasakawa, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Thermotabilization and thermocyclization of thermolabile enzymes by chitosane and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details. Location/Qualifiers 1..523 /organism="Mus musculus" /db_xref="taxon:10090" /clone_id="A930106009" /clone_lib="RIKEN full-length enriched, adult retina" /tissue_type="retina"		

REFERENCE 1 (bases 1 to 588)
AUTHORS Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Caeas, E.,
Stone, R.T., Heaton, M.P., Grose, W.M., Bennett, G.A., Laegreid, W.W.,
and Keele, J.W.

TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine

JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.

PCR primers

FORWARD: AGAAGACAGCTATGACCAT
BACKWARD: GTTTCAGTCAGCAGC
Plate: 141 row: 1 column: 23
Seq primer: ATTTAGTGACACTATAG.

FEATURES

source

1..588

/organism="Sus scrofa"

/db_xref="taxon:9823"

/clone_lib="MARC 2P1G"

/issue_type="pooled"

/lab_host="DH10B"

/note="Vector: PCMV SPOR6; Site 1: NotI; Site 2: SalI;
library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 146 a 151 c 165 g 126 t
ORIGIN

Query Match

Best Local Similarity 81.2%; Score 352; DB 13; Length 588;

Matches 409; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

```
QY 1 GTGGCCAGTGGCCGGGCGCATGTTGCTAGTGTGCTGATCTTGCTGCTGATGCTGACAGAGC 60
Db 47 GCGGGAAGTGGCCCGGCGATGTTACTAGTGTGCTGAGCCTGGCCGGCTGTGCTGGGCT 106
QY 61 GCCCTGCTGAGAGCCGACTATTCACTGTGCTCTGAGACAGGGCCATCTCCAGAGTGG 120
Db 107 GCCATGCTCTCCAGAGCCGACAAATTCAGTGTGCTGAGCCTGAGCTGTCTCCAGATGG 166
QY 121 ATGGTCCAGACACACTCACTCCAGAGACTTGAGGAGACCTCCAGTGAACCTGCTCAAG 180
Db 167 ATGGGTGACAGCCTCTGACCCGAGGAGACTTGAGGAGACCTCCAGTGAACCTATTAA 226
QY 181 ACAAGTGGGACAGAGAGATTTCATTTGATGAAACATAAGCTGATATCCGGGCA 240
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Job time : 3619.13 secs

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OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 23:34:39 ; Search time 290.439 Seconds
(without alignments)
11770.723 Million cell updates/sec

Title: US-09-778-971-4

Perfect score: 2589
Sequence: 1 gtggccagtgccggccat.....aaaaaaaaaaaaaaaaaaaa 2589

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 828747 seqs, 66023138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	644.8	24.9	1796	9	US-09-863-818A-1
4	643.2	24.8	1827	10	US-09-778-971-1
5	643.2	24.8	1841	10	US-09-886-404-17
6	643.2	24.8	2015	10	US-09-886-404-19
7	632.2	24.4	637	9	US-09-863-818A-3
8	625.6	24.2	1515	9	US-09-874-503-11
9	625.6	24.2	1515	9	US-10-000-157-11
10	625.6	24.2	1515	9	US-10-063-547-157
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ALIGNMENTS

RESULT 1
US-09-778-971-4
Sequence 4, Application US/09778971
Patent No. US20020102639A1
GENERAL INFORMATION:
APPLICANT: Shaughnessy, John D.
TITLE OF INVENTION: Ev127 Gene Sequence and Protein Encoded Thereby
FILE REFERENCE: D6138
CURRENT APPLICATION NUMBER: US/09/778, 971
PRIOR APPLICATION NUMBER: 2001-02-02
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 4
LENGTH: 2589
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: prim transcript
OTHER INFORMATION: cDNA of mouse Ev127
US-09-778-971-4

Query Match	100.0%	Score 2589;	DB 10;	Length 2589;
Best Local Similarity	100.0%	Pred. No. 0;		
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QY	121	ATGCTCAACACACTCACTCCAGAGACTTGAGGAGCCTCCAGTGAATCTGCTCAAG	180	
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RESULT 2

US-09-778-971-3
Sequence 3, Application US/09778971
Patent No. US20020102639A1
GENERAL INFORMATION:
APPLICANT: Shaughnessy, John D.
TITLE OF INVENTION: Ev127 Gene Sequence and Protein Encoded Thereby
FILE REFERENCE: D6138
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/180,374
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 3
LENGTH: 1963
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: prim.transcript
OTHER INFORMATION: cDNA of mouse Ev127
US-09-778-971-3

Query Match 56.9%; Score 1472.2; DB 10; Length 1963;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 2553 GCTTTGGAGGCTCTCAAAAAA 2589
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RESULT 3

US-09-863-818A-1
Sequence 1, Application US/09863818A
Publication No. US20030092881A1

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; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DKO170K
; CURRENT APPLICATION NUMBER: US/09/863,818A
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(1509)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (46)..()
; OTHER INFORMATION:
; US-09-863-818A-1

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Query Match      24.9%; Score 644.8; DB 9; Length 1796;
Best Local Similarity 76.0%; Pred. No. 6.6e-200;
Matches 853; Conservative 0; Mismatches 252; Indels 17; Gaps 4;

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Qy 1173 GGAAGCTGTGGGACCGAGACATCATCTGTTGTAAGAAAGAGAGATGTTGAAGT 1232
Db 532 GGAAGCTGTGGGACCGAGACATCATCTGTTGTAAGAAAGAGAGATGTTGAAGT 591
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Db 712 ATTCAGTGAAGTGGGATGATGAGAGTGTACGCTGAGTGAAGTGAAGTGAAGTGAAGT 771
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Db 772 TGTGGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 831
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Db 1009 GTGGTTATCTCTCTGATATGTTTCCATCAACGCTGTGCTCTCTCTCTCTCTCTCTCT 1068
Qy 1701 CAAAATCTACTGAGAGTGAAGTCTCTTGAATAATGAGAGAGAGAGAGAGAGAGAGAG 1760
Db 1069 CAAAATCTACTGAGAGTGAAGTCTCTTGAATAATGAGAGAGAGAGAGAGAGAGAGAG 1128
Qy 1761 ATGGGGCGGTACAGTGTGACCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1820

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Db 1129 ATGGGTCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1188
Qy 1821 CTTCCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1880
Db 1189 CTTCCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1248
Qy 1881 AGGAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1940
Db 1249 AGTGAAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1308
Qy 1941 AGCCAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2000
Db 1309 AGCCAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1368
Qy 2001 GACTATATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2060
Db 1369 GACTATATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1428
Qy 2061 CACAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2120
Db 1429 CACAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1488
Qy 2121 CAGATAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2178
Db 1489 CAGATAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1548
Qy 2179 TACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2220
Db 1549 TACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1590

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US-09-778-971-1
; Sequence 1, Application US/09778971
; Patent No. US20020102639A1
; GENERAL INFORMATION:
; APPLICANT: Shaughnessy, John D.
; TITLE OF INVENTION: Ev127 Gene Sequence and Protein Encoded Thereby
; FILE REFERENCE: D6138
; CURRENT APPLICATION NUMBER: US/09/778,971
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/180,374
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 1
; LENGTH: 1827
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: prim_transcript
; OTHER INFORMATION: cDNA of human Ev127
; US-09-778-971-1

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Query Match      24.8%; Score 643.2; DB 10; Length 1827;
Best Local Similarity 75.9%; Pred. No. 2.2e-199;
Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;

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Qy 1113 TTTCATTCCAGGCTGCTTAACACGATATGAATTAATAAGCTGACGTGAGCG 1172
Db 474 TTTCATTCCAGGCTGCTTAACACGATATGAATTAATAAGCTGACGTGAGCG 533
Qy 1173 GGAAGCTGTGGGACCGAGACATCATCTGTTGTAAGAAAGAGAGATGTTGAAGT 1232
Db 534 GGAAGCTGTGGGACCGAGACATCATCTGTTGTAAGAAAGAGAGATGTTGAAGT 593
Qy 1233 AATTTCACAACCATTCCTCTTGGAAACAGATACAGATTCTCATCAACGGGACACACA 1292
Db 594 AACTTCACAACCATTCCTCTTGGAAACAGATACAGATTCTCATCAACGAGCACTATC 653
Qy 1293 TTGGGGTTTCTTAGAGTCTGG-----AGATAAATGATGAGAGACGTCTGTAGCC 1343
Db 654 ATGGGGTTTCTTAGAGTCTGG-----AGATAAATGATGAGAGACGTCTGTAGGTG 713

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; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
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; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 11
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-874-503-11

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Query Match      24.2%; Score 625.6; DB 9; Length 1515;
Best Local Similarity 77.1%; Pred. No. 1.1e-193;
Matches 805; Conservative 0; Mismatches 224; Indels 15; Gaps 3;

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QY 1113 TTTCATTCCAGGCTGCTTAACAGTATGTAATTAATAAGAGAGTGCATGAGGCG 1172
DB 475 TTTCCTCACCAGGCTGCTTAACAGTATGTAATTAATAAGAGAGTGCATGAGGCG 534
QY 1173 GGAAGCTGTGGGAGCCAGACATCATCTGCTTTAAAAAGAACGAGAGATGTTGAAGT 1232
DB 535 GGAAGCTGTGGGAGCCAGACATCATCTGCTTTAAAAAGAGATGAGAGACATGAGAGT 594
QY 1233 AATTTCACAAACATCCCTTGGAAACAGATACAGATTTCTTCAATCAACGGGACACACA 1292
DB 595 AACTTCACAAACATCCCTTGGAAACAGATACAGATTTCTTCAACAGACATATC 654
QY 1293 TTGGGGTTTCTAGAGTCTG-----AGATTAACATGATGAGAGAGTGTATGCC 1343
DB 655 ATGGGGTTTCTAGAGTCTG-----AGATTAACATGATGAGAGAGTGTATGCC 714
QY 1344 ATCCGGTGAAGAGAGTGAAGTGGCGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1403
DB 715 ATTCAGATGAGTGGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 774
QY 1404 TGGGCGCATGATGATCCGACGCGAAGGAGCACTTGTGCTTGTGCTGAGAGCAAGTCT 1463
DB 775 TGGGCGCATGATGATCCGACGCGAAGGAGCACTTGTGCTGCTGCTGCTGCTGCTGCT 834
QY 1464 CCATCCCTCAGATGACAGACGAGATGCTGGGAGGCTGGGAGGCTGCTGCTGCTGCTGCT 1523
DB 835 CTTTCCCTCAGATGACAGACGAGATGCTGGGAGGCTGGGAGGCTGCTGCTGCTGCTGCT 894
QY 1524 ---CTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1580
DB 895 TCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 954
QY 1581 AGGAGCAGAGAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1640
DB 955 AGGATCAAGAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1011
QY 1641 GTGGTTTATCTTCTGATATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1700
DB 1012 GTGGTTTATCTTCTGATATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1071
QY 1701 CAAATCTAGCAGAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1760
DB 1072 CAAATCTAGCAGAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1131
QY 1761 ATGGGGCGGATGAGTGTGACCACTCAGAGAGCAAGCGGAGATTAAGTGTCTTCTTCT 1820

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DB 1132 ATGGGTCAGATGAGTGTGCTTGGCACTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1191
QY 1821 CTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1880
DB 1192 CTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1251
QY 1881 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1940
DB 1252 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1311
QY 1941 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2000
DB 1312 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1371
QY 2001 GACTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2060
DB 1372 GATTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1431
QY 2061 CACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2120
DB 1432 TGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1491
QY 2121 CATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2144
DB 1492 CACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1515

RESULT 9
US-10-000-157-11
; Sequence 11, Application US/10000157
; Publication No. US20020182673A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul L.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austen
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah
; APPLICANT: Tumaz, Daniel
; APPLICANT: Starovansnik, Melissa.
; APPLICANT: Vanhookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P138131P4 (US)
; CURRENT APPLICATION NUMBER: US/10/000,157
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/172096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/175481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191007
; PRIOR FILING DATE: 2000-03-21

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PRIOR	APPLICATION NUMBER:	60/213807
PRIOR	FILING DATE:	2000-06-22
PRIOR	APPLICATION NUMBER:	60/242837
PRIOR	FILING DATE:	2000-10-24
PRIOR	APPLICATION NUMBER:	60/244072
PRIOR	FILING DATE:	2000-10-26
PRIOR	APPLICATION NUMBER:	60/253546
PRIOR	FILING DATE:	2000-11-28
PRIOR	APPLICATION NUMBER:	09/311932
PRIOR	FILING DATE:	1999-05-14
PRIOR	APPLICATION NUMBER:	09/380138
PRIOR	FILING DATE:	1999-08-25
PRIOR	APPLICATION NUMBER:	09/380142
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PRIOR	APPLICATION NUMBER:	09/644848
PRIOR	FILING DATE:	2000-08-22
PRIOR	APPLICATION NUMBER:	09/747259
PRIOR	FILING DATE:	2000-12-20
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PRIOR	FILING DATE:	2001-03-22
PRIOR	APPLICATION NUMBER:	09/854208
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PRIOR	APPLICATION NUMBER:	09/854280
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PRIOR	APPLICATION NUMBER:	09/874503
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PRIOR	APPLICATION NUMBER:	PCT/US00/152644
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PRIOR	APPLICATION NUMBER:	PCT/US00/308733
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PRIOR	APPLICATION NUMBER:	PCT/US00/349566
PRIOR	FILING DATE:	2000-12-20
PRIOR	APPLICATION NUMBER:	PCT/US01/065200
PRIOR	FILING DATE:	2001-02-28
PRIOR	APPLICATION NUMBER:	PCT/US01/178000
PRIOR	FILING DATE:	2001-06-01
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PRIOR	APPLICATION NUMBER:	PCT/US01/210666
PRIOR	FILING DATE:	2001-06-29
PRIOR	APPLICATION NUMBER:	PCT/US01/217355
PRIOR	FILING DATE:	2001-07-09
SEQ ID NO 11	NUMBER OF SEQ ID NOS:	39
LENGTH:	1515	
TYPE:	DNA	
ORGANISM:	Homo Sapien	

	Query Match	24.2%	Score 625.6;	DB 9;	Length 1515;
	Beet Local Similarity	77.1%;	Pred. No. 1.1e-19;		
	Matches 805;	Conservative	0;	Mismatches 224;	Indels 15; Gaps
QY	1113 TTTCATTTCCAGGCTCCTTAACCGATGAATAAATTAAATGAACAAGCACTGAAGGC	1172			
DB	475 TTCACTTCAACAAGGCTCCTTAGAACCACTAATGAAATATAAAAAAAAGTGTCMAAGGCC	534			
QY	1173 GGAAGCCTGTGGAGCCAGA CATCATCTGCTTGTA AAAAACAAGAAAGATGGTTGAAGTG	1232			
DB	535 GGAAAGCTGTGGGATTCGGAACATCATCTGCTTGTAAGAAAGATGAAGAAACAGTAGAAGTG	594			
QY	1233 AATTTCACAAACCAATCCCTTGGAAAAAGATACAGATTTCTCATTC AACGGGACAGCA	1292			
DB	595 AACTTCACAAACCACTCCCCTGGGAAAAGATATCATGGCTCTTATCCAAACAGCACTATAC	654			
QY	1293 TTGGGGTTTTCTAAGATGCTGG-----NGAATAAATGATAGACGCTGTGAGCC	-1343			
DB	655 ATCCGGTTTTCTCAGGCTTTTGAAGCAACACAGAAAMAAACAAACCGAGCTTCAGTGTGTG	714			
QY	1344 ATCCCGGGA CTAGAGAGATGAAGGAGGGGTTCAGCTGACCCATATTTCAATACC	1403			
DB	715 ATTCAAGTACTGGGGATAGGAAGGTGCTAGGTGCACTACTCATATTTTCTACT	774			
QY	1404 TCGCGCATGACTGATCCGACCGGAAGGACAGTTGTGCTTGTCTCAGACAAATGCT	1463			
DB	775 TGTTGCGACGCACTGCATTCGACATAAAGGAACGTTGTGCTGTGCCCAAACAGGCGTC	834			
QY	1464 CCATTCCTTCCAATGACAAACAGACGATGCTGGAGGCTGGCTGCTCTCTCTGTGTG	1523			
DB	835 CTTTTCCTCTGATTAACAACAAAGCAAGCGGGAGGCTGCTGCTCTCTCTCTGTGTG	894			
QY	1524 ---CTGCGTGGGTGTGTGTGGGTGCTGGGACTGAGATCTACTAATTTGAGGACAAAGCA	1580			
DB	895 TCTCTGCTGGGTGGCACATAGGTGTGTGGGACGGGATTAATCTAATGTGAGGAGCAAA	954			
QY	1581 AGGAGACGAAGAAGTCTCTTCTATTTTCCACCATGCTCTGCCCCCATTTAAGTCTGTG	1640			
DB	955 AGGATCAAGAAAGACTTCTTTTCTA---CCACCAACCTATCTGCCCCCATTTAAGTCTTT	1011			
QY	1641 GTGTGTTATCCTTCTGAGATATGTTTCACTACACCGTGTGTGCTTCACTGACTTTCTT	1700			
DB	1012 GTGTGTTATCCCATCTGAATATATGTTTCCATACACAAATTTGTTACTTCACTGAATTTCTT	1071			
QY	1701 CAATACTATCTCAGAGTGAAGTCACTCTTTGA AAAATGSCAGAAAAGAAATGCGCAG	1760			
DB	1072 CAATAACCTATGCAAAAGTGAAGTCACTCTTTGA AAAGTGCAAAAAAATAATGACAG	1131			
QY	1761 ATGGGGCCGGATCAGGTGGCTGAACA CTCGAAGAACAGGGGAGATAAAGTGTCTTCTT	1820			
DB	1132 ATGGGTTCAGTGCAGGTGGCTTGCACCTCAAAAGAAAGACAGCAAAAGTGTCTTCTT	1191			
QY	1821 CTTCACAGTACGTCCCGGACCCCTTGTGCAAGTGCCTGTGGCAATAGAGGGAGCGCC	1880			
DB	1132 CTTTTCCATATGACGTCAACAGTGTGTGCAATGTGTA ACTGTGGCAABAGGAGGCACTGCC	1251			
QY	1881 AGGAGAACTCTCAGATCTGTTCCTCTTTCCTTAACCTCTTTTGTATGATTTACG	1940			
DB	1252 AGTGAAGACTCTCAAGACCTCTTCCCTTGGCTTTAATCTTTTCTGACGTATCTAAGA	1311			
QY	1941 AGCCAGACGATCTGCAAAATACCTGTGTGTCTAATCTTTGGGGGAGCAACTCAAGGC	2000			
DB	1312 AGCCAGATTAATCTGCAAAATAGTGTGTCTACTTTAAGAGATTTGAACAAAGAC	1371			
QY	2001 GACTATATAGCCCTGAGTGTCTGCCCCCAATATCAATCTCATAGAGAGCGCACAGCTTTC	2060			
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DB	1432 TGTCAGAACTTCTCCATGTCAAGACGAGGTGTGAGAGGAAAGATCAACAGCTGCG	1491			


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; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO: 11
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-747-259-11

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Query Match      24.2% Score 625.6; DB 9; Length 1515;
Best Local Similarity 77.1%; Pred. No. 1.1e-193;
Matches 805; Conservative 0; Mismatches 224; Indels 15; Gaps 3;

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QY 1113 TTCACATTCCTCCAGGCTGCTTAACGACGTATGAATATATAAAGAGAGCACTGAGGGG 1172
DB 475 TTCACCTCAGCAGGCTGCTTAACGACGTATGAATATATAAAGAGAGCACTGAGGGG 534
QY 1173 GGAAGCCTGTGGAGCCAGACATCACTGCTTTAAAGAGAGAGAGAGAGAGAGAG 1232
DB 535 GGAAGCCTGTGGAGCCAGACATCACTGCTTTAAAGAGAGAGAGAGAGAGAGAG 594
QY 1233 AATTTCACACCAATCCCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1292
DB 595 AACTTCACACCAATCCCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 654
QY 1293 TTGGGGTTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1343
DB 655 ATGGGTTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 714
QY 1344 ATCCCGTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1403
DB 715 ATTTCAGTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 774
QY 1404 TGGCGCATGACTGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1463
DB 775 TGGCGCATGACTGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 834
QY 1464 CCATCCCTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1523
DB 835 CTTTCCCTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 894
QY 1524 ---CTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1580
DB 895 TCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 954
QY 1581 AGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1640
DB 955 AGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1011
QY 1641 GTGGTTTATCTTGGATGATGTTTCCATCAACGCTGCTGCTTCACTTCACTTCTT 1700
DB 1012 GTGGTTTATCTTGGATGATGTTTCCATCAACGCTGCTGCTTCACTTCACTTCTT 1071

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QY 1701 CAAACTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1760
DB 1072 CAAACCATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1131
QY 1761 AAGGGGCGGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1820
DB 1132 ATGGGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1191
QY 1821 CTTCCAGTGGAGTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1880
DB 1192 CTTCCAGTGGAGTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1251
QY 1881 AGGAGAGACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1940
DB 1252 AGTGAAGAGACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1311
QY 1941 AGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2000
DB 1312 AGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1371
QY 2001 GACTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2060
DB 1372 GACTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1431
QY 2061 CACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2120
DB 1432 TGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1491
QY 2121 CATGATAGCTGCTTCACTCTTGTAG 2144
DB 1492 CACGATAGCTGCTTCACTCTTGTAG 1515

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RESULT 12
US-10-174-590-399
; Sequence 399, Application US/10174590
; Publication No. US2003008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Macanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-399

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Query Match      24.2% Score 625.6; DB 9; Length 1515;
Best Local Similarity 77.1%; Pred. No. 1.1e-193;
Matches 805; Conservative 0; Mismatches 224; Indels 15; Gaps 3;

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QY 1821 CTTCCAGTACGTCCTCCGACCCCTTGTGACAGTGCCTGTGCGCAATGAGGCGAGCGCC 1880
 DB 1192 CTTTCCAAAGAGTGAAGAGTGTGTGCGATGTGACCTGTGCGAAGGCGAGGCGAGTCCC 1251
 QY 1881 AGGAGAACTCTCAGAGATCTGTTCCTCTTGCCTTTAACTCTTTGTGATGATTTACAGC 1940
 DB 1252 AGTGGAACTCTCAAGACCTCTTCCCTTGTGCTTTTAACTTTTGTGAGATCTTAAGA 1311
 QY 1941 AGCCAGAGCATCTGACAAATACCTGTGTATCTTGTGGGAGACAGACCTCAAGGCG 2000
 DB 1312 AGCCAGATTCATCTGCAAAATACGTGTGTCTACTTTAGAGAGATTGATACAAAGAGC 1371
 QY 2001 GACTTAATGCTGAGTGTCTGCCCCCAATATCATCTCATGAGAGCGCCAGCTTTC 2060
 DB 1372 GATTCAATGCTGTACGTGTCTGCCCCAGTAGACCATCTCATGAGAGATGCGACTTTC 1431
 QY 2061 CACACAGAACTTCTCAGGCTACGAGAGCATCTCAGTGAAGAACTCTCAAGCTTGC 2120
 DB 1432 TGTGCAAACTTCTCATGTCAAGCAGGTGTGACAGAGAAAGATCACAGCTTGC 1491
 QY 2121 CATGATAGCTGTTCACCTTTAG 2144
 DB 1492 CACGATGCTGTCTCTCTTTAG 1515

RESULT 14

US-10-063-616-157
 ; Sequence 157, Application US/10063616
 ; Publication No. US20030013855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Balton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECURED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,616
 ; CURRENT FILING DATE: 2002-05-03
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 157
 ; LENGTH: 1515
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-063-616-157

Query Match 24.2% Score 625.6; DB 9; Length 1515;
 Best Local Similarity 77.1%; Pred. No. 1.1e-193;
 Matches 805; Conservative 0; Mismatches 224; Indels 15; Gaps 3;

QY 1113 TTCACTTCCAGGCTGCTTAAACCGATATGAAATATTAAGAGTGCAGTGGCG 1172
 DB 475 TTCACTTCCAGGCTGCTTAAACCGATATGAAATATTAAGAGTGCAGTGGCG 534
 QY 1172 GGAAGGCTGTGGGACCCAGACATCACTGCTTGTAAAGAGAGAGAGTGGTGAAGTG 1232
 DB 535 GGAAGGCTGTGGGATCGAATCATCACTGCTTGTAAAGAGAGAGAGTGAAGTG 594
 QY 1233 AATTTCACCAACCAATCCCTTGGAAACAGATACAGATTCTCATTTCAACGGGACAGACA 1292
 DB 595 AACTTCACCAACCACTCCCTGGGAAACAGATACATGCTCTTATTCACACAGCACTATAC 654
 QY 1293 TTGGGGTTTCTAGAGTGTCTG-----AGATTAATCTGATGAGAGCTGTGAGCC 1343
 DB 655 ATCGGGTTTCTAGAGTGTGAGCCACACAGAGAAACAAACGGAGCTTCAAGTG 714

QY 1344 ATCCGGTACTAGAGAGAGTGAAGTGGGTGTGCTTCACTGACCCCATATTTTACATACC 1403
 DB 715 ATTCAGTACTAGGGGATAGTGAAGTGTCTACGATGACCTGATCTCATATTTTCTTACT 774
 QY 1404 TCGGCAATGATCTGATCTCGAGCGGAGGAGACATTTGTCTTTGCTCAAGACATGTCT 1463
 DB 775 TGTGGCAGGACTGTGATCGACATTAAGGAGCATTTGTCTGTGCCCAAAACAGGCTTC 834
 QY 1464 CCCATCCCTCCAGATGACAAACAGACATCTGGGAGGCTGGCTGCTCTTCTCTGATG 1523
 DB 835 CTTTTCCTCTGATATACAAACAAAGACCGGAGGCTGGCTGCTCTCTCTGCTG 894
 QY 1524 ---CTGTGTGCTGT 1580
 DB 895 TCTGT 954
 QY 1581 AGGAGCAGAAACGTCCTTTCTTATTTTCACATGCTCTGCTCTCTTATTAAGTCTG 1640
 DB 955 AGGATCAAGAAACCTTCTTCTA---CCACCACTACTGCCCCCAATTAAGTCTT 1011
 QY 1641 GTGTTTTTACCTTGTGATATGTTTTCATACACCGTGTGTGTGTGTGTGTGTGTGTGT 1700
 DB 1012 GTGTTTTTACCTTGTGATATGTTTTCATACACATTTGTACTTCACTGATTTCTT 1071
 QY 1701 CAAACTACTGCAAGAGTGAAGTCTCTTGAAGAAATGCGAGAAATGCGCGAG 1760
 DB 1072 CAAACCAATGCAAGAGTGAAGTCTCTTGAAGAAATGCGAGAAATGCGCGAG 1131
 QY 1761 ATGGGCGGTGACGTGTGTGACCACTGAGAAACAGCGGCGATTAAGTGTCTTCTT 1820
 DB 1132 ATGGGTTCAGT 1191
 QY 1821 CTTCCAGTACGTCCTCCGACCTTGTGTGACGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1880
 DB 1192 CTTTCAATGACGTCAAGAGT 1251
 QY 1881 AGGAGAACTCTCAGAGATCTTTCCTCTTGTGCTTTTAACTCTTTGTGATGATTTACAGC 1940
 DB 1252 AGTGAAGACTCTCAAGACCTTCTCCCTGTGCTTTTAACTTTTGTGAGTATCTAAGA 1311
 QY 1941 AGCCAGAGCATCTGCAAAATACCTGTTGTCTTCTTTGGGAGAGCACTCAAGGCG 2000
 DB 1312 AGCCAGATTCATCTGCAAAATACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1371
 QY 2001 GACTTAATGCTGAGT 2060
 DB 1372 GATTCAATGCTGTCAAGT 1431
 QY 2061 CACACAGAACTTCTCAGGCTACGAGAGCATGTCTGTAAGAAACGCTCAAGCTTGC 2120
 DB 1432 TGTGCAAACTTCTCATGTCTCAAGAGCAGGTGTCTCAGCAGGAAAGATCACAGCTTGC 1491
 QY 2121 CATGATAGCTGTTCACCTTTAG 2144
 DB 1492 CACGATGCTGTCTCTCTTTAG 1515

RESULT 15

US-10-175-737-399
 ; Sequence 399, Application US/10175737
 ; Publication No. US20030013153A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin

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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: us/10/175, 737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 399
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-737-399

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Query Match      24.2%; Score 625.6; DB 9; Length 1515;
Best Local Similarity 77.1%; Pred. No. 1,1e-193;
Matches 805; Conservative 0; Mismatches 224; Indels 15; Gaps 3;

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QY 1113 TTTCATTTCCAGGCTGCTTAACCAAGTATGAAATATTAAGAGCTGACTGAGCGC 1172
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 475 TTTCATTTCCAGGCTGCTTAACCAAGTATGAAATATTAAGAGCTGACTGAGCGC 534

QY 1173 GGAAGCTGTGGAGCCAGACATCATGCTTTGTAAGAAAGAGAGATGTTGAAGTG 1232
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 535 GGAAGCTGTGGAGCCAGACATCATGCTTTGTAAGAAAGAGAGATGTTGAAGTG 594

QY 1233 AATTTCACAACCAATCCCTTGGAAACAGATACAGATTCTATTCAACGGGACAGACA 1292
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 595 AACTTCACAACCAATCCCTTGGAAACAGATACAGATTCTATTCAACAGACATATC 654

QY 1293 TTGGGGTTTCTAGAGTGTG-----AGATTAAGTATGAGAGCTGTAGCC 1343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 655 ATGGGGTTTCTAGAGTGTG-----AGATTAAGTATGAGAGCTGTAGCC 714

QY 1344 ATCCCGGTGACTGAGAGAGTGAAGTGGGTGTTGAGTGAACCCCATATTTATACACC 1403
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 715 ATTCCAGTACTGGGGATATGAAAGTGTACAGTGTGACTGACTCATATTTTCTACT 774

QY 1404 TGGGGCAATGACTGATCCGACGCGAAAGGACAGTTGTGCTTGTGTCAGACAAAGTCT 1463
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 775 TGTGGCAGCGACTGATCCGACATTAAGAAAGAGTGTGCTGTCACAAACAGCGCTC 834

QY 1464 CCCATCCCTCCATGATGACACAGACGATGCTGGAGAGCTGCTGCTCTTCTGTGTG 1523
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 835 CTTTCCCTCTGATTAACAAACAAAGAGCCGGAGGCTGCTCTCTCTGCTG 894

QY 1524 ---CTGCTGTGCTGTGTGGGTGCTGGAGCTGGAGTCTACCTTAAGGCAAGGA 1580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 895 TCTCTGTGTGTGGCAGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 954

QY 1581 AGGAGCAGAAAGCTCTTTCTATTTCACCAATGCTCTGCCCCCATTAAGTCTTG 1640
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 955 AGGATCAAGAAAGCTCTTTCTATTTCACCAATGCTCTGCCCCCATTAAGTCTTG 1011

QY 1641 GTGTTTATCTTCTGTGATATGTTTCCATCAACCGTGTGTGCTTCACTGACTTTCTT 1700
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1012 GTGTTTATCTTCTGTGATATGTTTCCATCAACCAATGTTTAACTTCACTGAATTTCTT 1071

QY 1701 CAAAACACTGACAGAAAGTGAAGTCACTCTTGAAGAAATGGCAGAAAGAAATGCCGAG 1760
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1072 CAAAACACTGACAGAAAGTGAAGTCACTCTTGAAGAAATGGCAGAAAGAAATGGCAGAG 1131

QY 1761 ATGGGGCCGGGTACAGTGTGACCTCAGAACCAAGCGGACAGTAAAGTGTCTTCTT 1820
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1132 ATGGGTTCAGTGAAGTGTGCTTGCACATAAAGAGGACAGACAAAGTGTCTTCTT 1191

QY 1821 CTTCCCAAGTACGTCGCGACCTTTTGTGACAGTGTGTGTGCAATGAGGCAAGCGCC 1880
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1192 CTTTCAATGACGTCAACAGTGTGTGTGATGATCTGTGTGCAAGCGGACAGTCTCC 1251

QY 1881 AGGAGAACTCTCAGAGATGTTTCCCTTGTGCTTAACTCTTTGTAGATTTCAAGC 1940
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1252 AGTGAAGTCTCTCAAGACTCTTCCCTTGTGCTTAACTCTTTTGTGAGTATTAAGA 1311

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QY 1941 AGCCAGACGATCTGCACAAATACCTGTGTGTCTATCTTGGGGAGCAGACTCAAGGC 2000
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1312 AGCCAGATCTCTGCACAAATACGTTGTGTCTACTTTAGAGATGATGATCAAAAGAC 1371

QY 2001 GACTATAAGCCCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2060
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1372 GATTACAAAGTCTCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1431

QY 2061 CACACAACTTCTCAAGCTACGACAGACATGTCAAGTGAAGAAAGCTCACAAAGCTTC 2120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1432 TGTGCAAGACTTCTCATGTCAAGCAGAGTGTCAAGCAAGAAAGATCACAAAGCTTC 1491

QY 2121 CATGATAGCTGTTCACCTTTGAG 2144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1492 CACGATGCTGTGTCTCTTTGAG 1515

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Search completed: May 28, 2003, 10:38:02
Job time : 332.439 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 23:31:59 / Search time 86.0664 Seconds
(without alignments)
9225.277 Million cell updates/sec

Title: US-09-778-971-4

Perfect score: 2589

Sequence: 1 gfgccagcgtgcccggccat.....aaaaaaaaaaaaaaaaa 2589

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 443362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	46.6	1.8	259	US-08-222-177A-24	Sequence 24, Appl
C 2	45.2	1.7	7218	US-08-232-463-14	Sequence 14, Appl
C 3	44.4	1.7	6953	US-07-805-123C-2	Sequence 2, Appl
C 4	44.4	1.7	6953	US-08-033-081B-2	Sequence 2, Appl
C 5	44.2	1.7	62	US-08-222-177A-56	Sequence 56, Appl
C 6	43.8	1.7	22846	US-08-469-461-3	Sequence 3, Appl
C 7	43.8	1.7	22846	US-07-890-609-3	Sequence 3, Appl
C 8	42	1.6	2529	US-09-051-969A-5	Sequence 5, Appl
C 9	41.2	1.6	2997	US-08-486-343A-3	Sequence 3, Appl
C 10	41.2	1.6	2997	PCT-US95-07349-3	Sequence 3, Appl
C 11	41.1	1.6	50	US-08-222-177A-169	Sequence 169, App
C 12	40.8	1.6	3854	US-08-720-484A-1	Sequence 1, Appl
C 13	40.8	1.6	3854	US-08-953-823A-1	Sequence 1, Appl
C 14	40.8	1.6	3854	US-09-398-239-1	Sequence 1, Appl
C 15	40.4	1.6	2360	US-08-916-043-3	Sequence 3, Appl
C 16	40.2	1.6	210	US-08-222-177A-23	Sequence 23, Appl
C 17	40	1.5	1083	US-09-177-650-121	Sequence 121, App
C 18	39.6	1.5	155	US-08-222-177A-19	Sequence 19, Appl
C 19	39.4	1.5	818	US-08-205-697A-4	Sequence 4, Appl
C 20	39.4	1.5	818	US-08-702-525-4	Sequence 4, Appl
C 21	39.4	1.5	818	PCT-US95-02576-4	Sequence 4, Appl
C 22	39.4	1.5	1570	US-08-205-697A-10	Sequence 10, Appl
C 23	39.4	1.5	1570	US-08-702-525-10	Sequence 10, Appl
C 24	39.4	1.5	1570	PCT-US95-02576-10	Sequence 10, Appl
C 25	39.4	1.5	1606	US-08-702-525-64	Sequence 64, Appl
C 26	39.4	1.5	1606	PCT-US95-02576-64	Sequence 64, Appl
C 27	39.4	1.5	1888	US-08-205-697A-1	Sequence 1, Appl

C 28	39.4	1.5	1888	US-08-702-525-1	Sequence 1, Appl
C 29	39.4	1.5	1888	PCT-US95-02576-1	Sequence 1, Appl
C 30	39.4	1.5	2516	US-08-205-697A-3	Sequence 3, Appl
C 31	39.4	1.5	2516	US-08-702-525-3	Sequence 3, Appl
C 32	39.4	1.5	2516	PCT-US95-02576-3	Sequence 3, Appl
C 33	39.2	1.5	190	US-08-222-177A-13	Sequence 13, Appl
C 34	39.2	1.5	1920	US-09-534-638-6	Sequence 6, Appl
C 35	39.2	1.5	9840	US-09-534-638-1	Sequence 1, Appl
C 36	39.2	1.5	11970	US-09-345-217-1	Sequence 1, Appl
C 37	39.2	1.5	152331	US-09-128-155-16	Sequence 16, Appl
C 38	39	1.5	2791	US-09-570-367C-1	Sequence 1, Appl
C 39	38.8	1.5	42	US-08-455-627-22	Sequence 22, Appl
C 40	38.8	1.5	42	US-08-689-856-22	Sequence 22, Appl
C 41	38.8	1.5	35100	US-08-306-691B-19	Sequence 19, Appl
C 42	38.8	1.5	35100	PCT-US93-06251-19	Sequence 19, Appl
C 43	38.8	1.5	80246	US-09-078-294-4	Sequence 4, Appl
C 44	38.8	1.5	80595	US-09-078-294-3	Sequence 3, Appl
C 45	38.8	1.5	90050	US-09-245-041-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-222-177A-24/c
Sequence 24, Application US/08222177A
Patent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dc-da)n. (dc-dt)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSER: Dewitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865, 601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: Caucasian
TISSUE TYPE: Blood
IMMEDIATE SOURCE:
CLONE: Mtd40
POSITION IN GENOME:

```

ADDRESS:  Foley & Lardner
STREET:  1800 Diagonal Road, Suite 500
CITY:    Alexandria
STATE:   VA
COUNTRY: USA
ZIP:     22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE:  Floppy disk
COMPUTER:  IBM PC compatible
OPERATING SYSTEM:  PC-DOS/MS-DOS
SOFTWARE:  Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER:  US/08/232,463
FILING DATE:
CLASSIFICATION:  435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:  US/07/935,313
FILING DATE:
APPLICATION NUMBER:  EP 91 114 300.6
FILING DATE:  26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME:  BENT, Stephen A.
REGISTRATION NUMBER:  29,768
REFERENCE/DOCKET NUMBER:  30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE:  (703)836-9300
TELEFAX:    (703)683-4109
TELEX:      899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH:  7218 base pairs
TYPE:  nucleic acid
STRANDEDNESS:  single
TOPOLOGY:  linear
IMMEDIATE SOURCE:
CLONE:  pTZgpc-Fl6
US-08-232-463-14

Query Match      1.7%; Score 45.2; DB 1; Length 7218;
Best Local Similarity 5.2%; Pred. No. 0.01;
Matches 20; Conservative 202; Mismatches 160; Indels 0; Gaps 0;

QY  330 CACAGAGGCGCTTCCAAACCCAGACCGACCTTCCGGCGCGCAATGAGATCTCTATGT 389
    |||||
DB  1020 CACAGAAATTAATTCGAGCTTGCGCTGCAGGTGAGGAGCTTGCGATYYYYYYYYYYY 1079
    :|||:
QY  390 AGGCTCCCTGGAGCGAGACACTCTATCTCATCTACGCCCCATATACCCCAATGC 449
    :|||:
DB  1080 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1139
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QY  450 TAAATATGAATGAGGACAGACCCCTCTTTGCTGTGAATCTACCTCGCAGAGGTGACTCG 509
    :|||:
DB  1140 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1199
    :|||:
QY  510 TGAACAACACAGAAGTAAGCTCCGGTGTATTTTCAGACAGCTAAACACACAGGCTTCGGAT 569
    :|||:
DB  1200 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1259
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QY  570 TTCAGCTCCTTCCCATATACAAATTTCCCTCGGGGCAAGAGACTCAGTCAATTCGCCACC 629
    :|||:
DB  1260 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1319
    :|||:
QY  630 CCAGCCTCTGCGCGTCTTTTTCATGACTTTGTCAACTTACCTAGCTTGTTCATCTCT 689
    :|||:
DB  1320 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1379
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QY  690 GAAATGTGTGATGCTTGCTTC 711
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DB  1380 YYYYYYYYYYYYYYYYYYYY 1401
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; Sequence 2, Application US/07805123C
; Patent No. 5262529
; GENERAL INFORMATION:
; APPLICANT: Dryja, Thadeus P.
; APPLICANT: Berson, Eliot L.
; TITLE OF INVENTION: DIAGNOSIS OF HEREDITARY RETINAL
; TITLE OF INVENTION: DEGENERATIVE DISEASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/805.123C
; FILING DATE: 19911211
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/469,215
; FILING DATE: January 24, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/069003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6953
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-805-123C-2

Query Match          1.7%; Score 44.4; DB 1; Length 6953;
Best Local Similarity 59.5%; Pred. No. 0.017;
Matches 75; Conservative 0; Mismatches 51; Indels 0; Gaps 0

QY 1020 GTAAGTGTGTTGGTGCTTTTGTGTGTGTGTGTGTGTGTGTACTGCGGAAG 1079
Db |-----|-----|-----|-----|-----|-----|-----|
QY 2116 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAACCA 2057
Db |-----|-----|-----|-----|-----|-----|-----|
QY 1080 GGTATTAACCTTACCACAATGTATACAACTTCATTCCATCCCAAGCTGCCTAACAC 1139
Db 2056 GCATCTAATGATGGGGCAGAGTTCCTGTGTGGGAAGCATGCAGAGTGTTGAAACCA 1997
QY 1140 GTAATG 1145
Db |---|---|
Db 1996 GAATG 1991

RESULT 4
US-08-033-081B-2/c
; Sequence 2, Application US/08033081B
; Patent No. 5498521
; GENERAL INFORMATION:
; APPLICANT: Dryja, Thadeus P.
; APPLICANT: Berson, Eliot L.
; TITLE OF INVENTION: DIAGNOSIS OF HEREDITARY RETINAL
; TITLE OF INVENTION: DEGENERATIVE DISEASES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street

```

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/ CITY: Boston  
/ STATE: Massachusetts  
/ COUNTRY: U.S.A.  
/ ZIP: 02110-2804  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
/ COMPUTER: IBM PS/2 Model 502 or 55SX  
/ OPERATING SYSTEM: MS-DOS (Version 5.0)  
/ SOFTWARE: WordPerfect (version 5.1)  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/033.081B  
/ FILING DATE: March 11, 1993  
/ CLASSIFICATION: 435  
/ PRIORITY APPLICATION DATA:  
/ APPLICATION NUMBER: 07/825.296  
/ FILING DATE: January 23, 1992  
/ APPLICATION NUMBER: 07/469,215  
/ FILING DATE: January 24, 1990  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Clark, Paul T.  
/ REGISTRATION NUMBER: 30,162  
/ REFERENCE/DOCKET NUMBER: 00246/069005  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (617) 542-5070  
/ TELEFAX: (617) 542-8906  
/ TEXTS: 200154  
/ INFORMATION FOR SEQ ID NO: 2:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 6953  
/ TYPE: nucleic acid  
/ STRANDEDNESS: double  
/ TOPOLOGY: linear  
US-08-033-081B-2
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Query Match          1.7%; Score 44.4; DB 1; Length 6953;  
Best Local Similarity 59.5%; Pred.No.0.017; Gaps 0,  
Matches 75; Conservative 0; Mismatches 51; Indels 0;
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Dy   1020 GTAAGTGTGCTGTGTTGGTGTCGTGTCGTGTCGTACTGGCAAAAG 1079  
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Db   2116 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAAGAAT 2057  
  
Dy   1080 GGTAATTACCTTACTCAAATGTACAATTCATTCCAGCGCTCCTAACCAC 1139  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db   2056 GCATCTCATATGCGGCAGAGTCTCTGTGTGAAGAAATCAGAGGTGTGAACCCA 1997  
  
Dy   1140 GTAATG 1145  
      ||||  
Db   1996 GAATTG 1991
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RESULT 5  
US-08-222-177A-56/C  
Sequence 56, Application US/08222177A  
Patent No. 5582979  
GENERAL INFORMATION:  
APPLICANT: Weber, James L.  
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN  
TITLE OF INVENTION: (IG-dA)n.(IG-dr)n SEQUENCES AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 460  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Demitl Ross & Stevens, S.C.  
STREET: 8000 Excelsior Drive, Suite 401  
CITY: Madison  
STATE: Wisconsin  
COUNTRY: USA  
ZIP: 53717-1914  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:
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; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dc-da)n.(dg-dt)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460

```

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ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3854 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-720-484A-1

Query Match      1.6%; Score 40.8; DB 2; Length 3854;
Best Local Similarity 81.9%; Pred. No. 0.14;
Matches 59; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Cy   998 TCTGTCGTCTCCATCATCTGAAGTACGTGCTGCTGCTGT -TTTGCTGCTGCTGCT
Db   3522 TCTCTTGAGACCACCACTCGAAGTAAGGGGTGTGTGTGTGTGTGTGTGTGTGT 3463
        |||||
Cy   1057 GTGTGTGTGTGT 1068
        |||||
Db   3462 GTGTGTGTGTGT 3451

RESULT 13
US-08-953-823A-1/c
Sequence 1, Application US/08953823A
Patent No. 6136958
GENERAL INFORMATION:
APPLICANT: Desauvage, Frederic
APPLICANT: Rosenthal, Arnon
APPLICANT: Stone, Donna
TITLE OF INVENTION: Vertebrate Smoothed Proteins
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,823A
FILING DATE: 30-Sep-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027070
FILING DATE: 30-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1050R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3854 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-953-823A-1

```


PR 04-FEB-2000; 2000US-0180374.
XX
XX (UVAR-) UNIV ARKANSAS.
XX
PI Shaughnessy JD;
XX
XX WPI; 2001-496920/54.
XX P-PSDB; AAE07163.
XX
PT New nucleic acids encoding an interleukin (IL)-17 receptor related
PT protein for use as a marker for leukemia
XX
XX Claim 1a; Page 77-78; 87bp; English.
XX
XX The present sequence is a cDNA encoding mouse interleukin (IL)-17
XX receptor related protein (Evi27). Mouse Evi27 gene was mapped to
XX chromosome 14. Evi27 is a common site of retroviral integration
XX in BXH2 murine myeloid leukaemias. Evi27 cDNA sequences are useful
XX as antisense molecules to inhibit Evi27 protein or for chromosomal
XX mapping or mutational analysis of Evi27 protein. They are proviral
XX integration sites associated with leukaemias and monitoring this
XX site provides a genetic tag for disease gene identification. The
XX proteins of the invention are useful to stimulate the secretion of
XX proinflammatory cytokines such as IL-8 and plays an important role
XX in the developmental and/or disease processes of haematopoietic
XX cells. Hence modulating the expression of Evi27 at the RNA or
XX protein level is used in the treatment of diseases such as cancer
XX or autoimmune diseases.
XX
XX Sequence 2589 BP; 642 A; 628 C; 643 G; 676 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 2589; DB 22; Length 2589;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GTGGCCAGTGGCCGGCCATGTTGCTAGTGTGCTGATCTTGCTGCATCGTGAGAGC 60
DB 1 GTGGCCAGTGGCCGGCCATGTTGCTAGTGTGCTGATCTTGCTGCATCGTGAGAGC 60
QY 61 GCCCTGCTCGAGAGCGGCACTATTCAGTGAGCTCTGAGACAGGGCCATCTCCAGAGTGG 120
DB 61 GCCCTGCTCGAGAGCGGCACTATTCAGTGAGCTCTGAGACAGGGCCATCTCCAGAGTGG 120
QY 121 ATGTGTCACACACACTCTCCAGAGACTTGAAGGAGCTTCAAGTGAAGTCTGTCAAG 180
DB 121 ATGTGTCACACACACTCTCCAGAGACTTGAAGGAGCTTCAAGTGAAGTCTGTCAAG 180
QY 181 ACAAGTGTGGACAGAGAGAGATTTCATTTTGAATGAATAGTGTGATCTCCGGGCA 240
DB 181 ACAAGTGTGGACAGAGAGAGATTTCATTTTGAATGAATAGTGTGATCTCCGGGCA 240
QY 241 GAGCCAGCATCCGCTTGTGAAGGCCCAAGATCTGCGGAGTGGGCAAAACAATG 300
DB 241 GAGCCAGCATCCGCTTGTGAAGGCCCAAGATCTGCGGAGTGGGCAAAACAATG 300
QY 301 AATTCAATACAGCTGTGAGGTGCACTACAGAGGCTTCAAAAGCAGACCAAGACT 360
DB 301 AATTCAATACAGCTGTGAGGTGCACTACAGAGGCTTCAAAAGCAGACCAAGACT 360
QY 361 TCCGGCGGCAATGAGACATTTCTTAATGTAGCTTCCCTGGAGCTGAGACACTCTAT 420
DB 361 TCCGGCGGCAATGAGACATTTCTTAATGTAGCTTCCCTGGAGCTGAGACACTCTAT 420
QY 421 CTCATCAGCGCCGCAATACATCCCAATGTCTAATGATGATGAGACAGCCCTCTTGTCT 480
DB 421 CTCATCAGCGCCGCAATACATCCCAATGTCTAATGATGATGAGACAGCCCTCTTGTCT 480
QY 481 GTGAACCTTCACTCGCAGAGGTGCACTGTGAAAAACAAGATGAAGTCCGGGTATTT 540
DB 481 GTGAACCTTCACTCGCAGAGGTGCACTGTGAAAAACAAGATGAAGTCCGGGTATTT 540
QY 541 CGAGAGCTAAACACAGAGCTCTCGGATTTGAGCTCTTCCATTTACATTTCTCTCT 600
DB 541 CGAGAGCTAAACACAGAGCTCTCGGATTTGAGCTCTTCCATTTACATTTCTCTCT 600

DB 541 CGAGAGCTAAACACAGAGCTCTCGGATTTGAGCTCTTCCATTTACATTTCTCTCT 600
QY 601 GGGCCAGAGGACTCAGTCAATTTGTCACACCCAGAGCTCTGAGCTTTCATGACTTT 660
DB 601 GGGCCAGAGGACTCAGTCAATTTGTCACACCCAGAGCTCTGAGCTTTCATGACTTT 660
QY 661 GTCAAACTTAAGCTTGTGTTTCCATTTGTAATTTGTCTGATGCTTGTGATGTAAG 720
DB 661 GTCAAACTTAAGCTTGTGTTTCCATTTGTAATTTGTCTGATGCTTGTGATGTAAG 720
QY 721 CCGGGGATAGAGTTTGGGTATGAATCCACAGAGGACCTGAATTTCTTCACTATGG 780
DB 721 CCGGGGATAGAGTTTGGGTATGAATCCACAGAGGACCTGAATTTCTTCACTATGG 780
QY 781 CCTATCGAGCTGTGTCACATTTGTTGAGGAGTGTGCTTACATGAGATCTGATCT 840
DB 781 CCTATCGAGCTGTGTCACATTTGTTGAGGAGTGTGCTTACATGAGATCTGATCT 840
QY 841 ACCACCTGAGCTTCATGCTGGAAGAGCAGAACCTATATGATTTGTGACCTTCACTT 900
DB 841 ACCACCTGAGCTTCATGCTGGAAGAGCAGAACCTATATGATTTGTGACCTTCACTT 900
QY 901 TTGTTTCCGTGTCACTCTCCGAGAGCTGTTTGTGATTAAGTGTGATTAAGAGATTA 960
DB 901 TTGTTTCCGTGTCACTCTCCGAGAGCTGTTTGTGATTAAGTGTGATTAAGAGATTA 960
QY 961 CTTAAAGCTTCCGTTGGAAGAGATGTTTCTATTAGATCTGTTGCTCATATCTGAAG 1020
DB 961 CTTAAAGCTTCCGTTGGAAGAGATGTTTCTATTAGATCTGTTGCTCATATCTGAAG 1020
QY 1021 TAAAGTGTGAGTGTGTTTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1080
DB 1021 TAAAGTGTGAGTGTGTTTGTGTTTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTT 1080
QY 1081 GTTATACCTTATCAAAATGTAACAATTTCATTCATTTCCAGAGCTGCTTAACCAAG 1140
DB 1081 GTTATACCTTATCAAAATGTAACAATTTCATTCATTTCCAGAGCTGCTTAACCAAG 1140
QY 1141 TAAATGAATTAATAAAGAGAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
DB 1141 TAAATGAATTAATAAAGAGAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
QY 1201 CTTGTAAAAAGAAAGAGAGATGTTGAAGTGAATTTCAACCAATCTCTTGAAGAA 1260
DB 1201 CTTGTAAAAAGAAAGAGAGATGTTGAAGTGAATTTCAACCAATCTCTTGAAGAA 1260
QY 1261 GATACAGATTTCAATTCACACGAGACACACATTTGGGGTTTCTAGAGTCTGGAATA 1320
DB 1261 GATACAGATTTCAATTCACACGAGACACACATTTGGGGTTTCTAGAGTCTGGAATA 1320
QY 1321 AACTGATGAGAGAGTCTGTAGCCATCCGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1380
DB 1321 AACTGATGAGAGAGTCTGTAGCCATCCGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1380
QY 1381 AGCTGACCCCAATTTTACATCTGCGGCAATGATCTGATCCGACGGAAGGAGACGTTG 1440
DB 1381 AGCTGACCCCAATTTTACATCTGCGGCAATGATCTGATCCGACGGAAGGAGACGTTG 1440
QY 1441 TGGTTTGTCAAGAGACAAAGTCTCCATCCCTCAATATACAAACACCATGTGAGAG 1500
DB 1441 TGGTTTGTCAAGAGACAAAGTCTCCATCCCTCAATATACAAACACCATGTGAGAG 1500
QY 1501 GCTGAGCTGCTCTCTCTGAGTCTGCTGAGGCTGTGAGGAGTGTGAGAGTGTGAGTCT 1560
DB 1501 GCTGAGCTGCTCTCTCTGAGTCTGCTGAGGCTGTGAGGAGTGTGAGAGTGTGAGTCT 1560
QY 1561 ACCTAACTTGAAGGCAAGAGAGAGACAGAACGTCCTTCTCTATTTTCAACATGCTCC 1620
DB 1561 ACCTAACTTGAAGGCAAGAGAGAGACAGAACGTCCTTCTCTATTTTCAACATGCTCC 1620
QY 1621 TGGCCCTCATTAAGTCTGTGAGTGTATTCCTTGTGAGATATGTTTTCATCAACGCTCT 1680
DB 1621 TGGCCCTCATTAAGTCTGTGAGTGTATTCCTTGTGAGATATGTTTTCATCAACGCTCT 1680

Qy	1681	GTCCCTTCACTGACTTTCTCTTCAAACTA	CTGCAAGAGTAGAGTCACTCTTGAAAAATGCG	1740	
Dp	1681	GTCCCTTCACTGACTTTCTCTTCAAACTA	CTGCAAGAGTAGAGTCACTCTTGAAAAATGCG	1740	
Qy	1741	AGAAAAAGAAAATGCGCGAGATGCGGCGGTA	CAGTGCTGACA	CTGAGAAACGACGCG	1800
Dp	1741	AGAAAAAGAAAATGCGCGAGATGCGGCGGTA	CAGTGCTGACA	CTGAGAAACGACGCG	1800
Qy	1801	CAGATTAAAGTGTCTTCCCTCTTCCAGATGAGT	CCCGACCCCTTGATCAGTGTCTGTG	1860	
Dp	1801	CAGATTAAAGTGTCTTCCCTCTTCCAGATGAGT	CCCGACCCCTTGATCAGTGTCTGTG	1860	
Qy	1861	GCCCAATGAGGGGAGCGCCAGGGAGAACTCT	CAGGATCTGTTCCTCTWGCTTTAAC	1920	
Dp	1861	GCCCAATGAGGGGAGCGCCAGGGAGAACTCT	CAGGATCTGTTCCTCTWGCTTTAAC	1920	
Qy	1921	TCCTTTGTAGTGAATTTGAGGACGACGAGCAT	GTGCACAAATACCTGGTGGTCTATCTTG	1980	
Dp	1921	TCCTTTGTAGTGAATTTGAGGACGACGAGCAT	GTGCACAAATACCTGGTGGTCTATCTTG	1980	
Qy	1981	GGGGAGCAGACCTTCAAAAGGGACTATTAATG	CCCTGAGTGTCTGCCCCCAATATCATCTCA	2040	
Dp	1981	GGGGAGCAGACCTTCAAAAGGGACTATTAATG	CCCTGAGTGTCTGCCCCCAATATCATCTCA	2040	
Qy	2041	TGAAGAGCGCACAGCTTTTCCACACAGAACTT	CTCAAGGCTACGAGAGCATGTCACTGA	2100	
Dp	2041	TGAAGAGCGCACAGCTTTTCCACACAGAACTT	CTCAAGGCTACGAGAGCATGTCACTGA	2100	
Qy	2101	AGAAACGCTCAACAAGCCTGCATGATAGCTGTT	CAACCTTGTAGTCA	CCCGGGGGAATA	2160
Dp	2101	AGAAACGCTCAACAAGCCTGCATGATAGCTGTT	CAACCTTGTAGTCA	CCCGGGGGAATA	2160
Qy	2161	GAGACTCTGAAGCCTTCTCTA	CTCTCCCTTCAGTGA	CAAAATGCTGTGAGAGCATCTGAA	2220
Dp	2161	GAGACTCTGAAGCCTTCTCTA	CTCTCCCTTCAGTGA	CAAAATGCTGTGAGAGCATCTGAA	2220
Qy	2221	ATGTGTGGGAGAGGCTGTGTGAGAGTAGTGA	CTATGTACAACTTGCTTTAAAACTGAGAT	2280	
Dp	2221	ATGTGTGGGAGAGGCTGTGTGAGAGTAGTGA	CTATGTACAACTTGCTTTAAAACTGAGAT	2280	
Qy	2281	TTGCAAAAGTCAACCTGAGCATACACCCCTGAG	CTAGTCAATGGCTGGAATTTATGAAGAC	2340	
Dp	2281	TTGCAAAAGTCAACCTGAGCATACACCCCTGAG	CTAGTCAATGGCTGGAATTTATGAAGAC	2340	
Qy	2341	AACACAGTTACAGACATTAATGAGTGGGAC	CTACATTTGGGATATACCCAAAGCTGGGTA	2400	
Dp	2341	AACACAGTTACAGACATTAATGAGTGGGAC	CTACATTTGGGATATACCCAAAGCTGGGTA	2400	
Qy	2401	ATGATTTATCACTGAGAACACGACACTGTGG	CCATGAAGTAAACCGCATCTCCGTCTAG	2460	
Dp	2401	ATGATTTATCACTGAGAACACGACACTGTGG	CCATGAAGTAAACCGCATCTCCGTCTAG	2460	
Qy	2461	GCTGTCTGTCAAGTGGGTGTGTTCTTGCA	CTGCCCATGCTCTATGCTGACGTAACCGT	2520	
Dp	2461	GCTGTCTGTCAAGTGGGTGTGTTCTTGCA	CTGCCCATGCTCTATGCTGACGTAACCGT	2520	
Qy	2521	TTTGTATCATTTTATCTGTATTAATGAATAT	CCGTTTGGGAAGCTCTCAAAAAAAAAAAAA	2580	
Dp	2521	TTTGTATCATTTTATCTGTATTAATGAATAT	CCGTTTGGGAAGCTCTCAAAAAAAAAAAAA	2580	
Qy	2581	AAAAAAA 2589			
Dp	2581	AAAAAAA 2589			
RESULT 2					
AADI3445					
ID	AADI3445 standard; cDNA; 1963 BP.				
XX	AADI3445;				
AC					
XX	06-NOV-2001 (first entry)				

Query Match	Best Local Similarity	Matches 1474; Conservative	Score 56.98; Pred. No. 0; Mismatches 0	Score 1472.2; DB 22; Length 1963; Indels 3; Gaps 0
1113	TTTCACATTC	CCGAGCGTGCTTAAACCA	CGTAAATGAAATATTA	AAAAAGCACTGCACTGAGGCG 1172
487	TTTCACTGCG	CCAGCGTGCTTAAACCA	CGTAAATGAAATATTA	AAAAAGCACTGCACTGAGGCG 546
1173	GAAGCGTGTGG	AGCCAGCATCATCTGCTT	GTAAAAAGAAAGAGAGAT	GGTTGAAGT 1232
547	GAAGCGTGTGG	AGCCAGCATCATCTGCTT	GTAAAAAGAAAGAGAT	GGTTGAAGT 606
1233	AATTTCACAA	CCCATCCCTTGAAACGAT	ATTCATTCACACGGACGCA	1292
607	AATTTCACAA	CCCATCCCTTGAAACGAT	ATTCATTCACACGGACGCA	666

QY 1293 TTGGGCTTTCTAGAGTCTGAGAAATAACTGATGAGAGCGTGTGAGCCATCCGGTG 1352
 Db 667 TTGGGCTTTCTAGAGTCTGAGAAATAACTGATGAGAGCGTGTGAGCCATCCGGTG 726
 QY 1353 ACTGAGAGAGGAAAGGCGGTGTGAGTGAAGCCCATTTTATGATACCTGGGGCAAT 1412
 Db 727 ACTGAGAGAGGAAAGGCGGTGTGAGTGAAGCCCATTTTATGATACCTGGGGCAAT 786
 QY 1413 GACTGATCCGACGCGAAGGAGCAGTTGCTTGTCTGAGAGACAAAGTCTCCATCCCT 1472
 Db 787 GACTGATCCGACGCGAAGGAGCAGTTGCTTGTCTGAGAGACAAAGTCTCCATCCCT 846
 QY 1473 CCAAGTGAACAACAGCGATGCTGGAGGCTGGCTCTTCTTCTGTGTGTGTGTG 1532
 Db 847 CCAAGTGAACAACAGCGATGCTGGAGGCTGGCTCTTCTTCTGTGTGTGTGTG 906
 QY 1533 GCTGTGGGGGCTGGGAGCTGGGATCTAATCTTGGAGGCAAGAAAGAGACGAG 1592
 Db 907 GCTGTGGGGGCTGGGAGCTGGGATCTAATCTTGGAGGCAAGAAAGAGACGAG 966
 QY 1593 ACGTCTTTCTTATTTCCACCATGCTCTGCCCCCTATTAAAGTCTGTGGTTTATCT 1652
 Db 967 ACGTCTTTCTTATTTCCACCATGCTCTGCCCCCTATTAAAGTCTGTGGTTTATCT 1026
 QY 1653 TCTGAGATATGTTTCATCAACCGTCTGTGCTTCACTGACTTCTTCAAACTACTGC 1712
 Db 1027 TCTGAGATATGTTTCATCAACCGTCTGTGCTTCACTGACTTCTTCAAACTACTGC 1086
 QY 1713 AGAAGTGAAGTATCTTGAAGAAATGCGAAGAAATGCGAAGTGGCGGTA 1772
 Db 1087 AGAAGTGAAGTATCTTGAAGAAATGCGAAGAAATGCGAAGTGGCGGTA 1146
 QY 1773 CAGTGTGACCACTCAGAAACCAAGCGGAGTAAAGTGTCTTCTTCCAGTAC 1832
 Db 1147 CAGTGTGACCACTCAGAAACCAAGCGGAGTAAAGTGTCTTCTTCCAGTAC 1206
 QY 1833 GTCCGACCTTTTGTGACAGTGTGTGCGCAATGAGGCGCGGAGAGAACTCT 1892
 Db 1207 GTCCGACCTTTTGTGACAGTGTGTGCGCAATGAGGCGCGGAGAGAACTCT 1266
 QY 1893 CAGATCTGTTCCCTCTTAACTCTTGTGATGATTTTCAAGCAAGCAACCAT 1952
 Db 1267 CAGATCTGTTCCCTCTTAACTCTTGTGATGATTTTCAAGCAAGCAACCAT 1326
 QY 1953 CTGACAAATACCTGTGTGTATCTTGGGGAGCAGACTCAAGGCGAATATATGCC 2012
 Db 1327 CTGACAAATACCTGTGTGTATCTTGGGGAGCAGACTCAAGGCGAATATATGCC 1386
 QY 2013 CTGAGTGTCTGCCCCCAATATCTCATGAGAGCGCACAGCTTTCCACAGAACTT 2072
 Db 1387 CTGAGTGTCTGCCCCCAATATCTCATGAGAGCGCACAGCTTTCCACAGAACTT 1446
 QY 2073 CTCAAGGCTACGAGAGATCTCAGTGAAGAAAGCTCAAGGCTCCATGATGCT 2132
 Db 1447 CTCAAGGCTACGAGAGATCTCAGTGAAGAAAGCTCAAGGCTCCATGATGCT 1506
 QY 2133 TCACCTTTAGTCCACCGGGGGAATAGAGACTCTGAAGCTTCTACTCTCCCTTCCA 2192
 Db 1507 TCACCTTTAGTCCACCGGGGGAATAGAGACTCTGAAGCTTCTACTCTCCCTTCCA 1566
 QY 2193 GTGACAAATGCTGTGAGCACTCTGAATGTGTGGAGAGAGGCTGTGTGAGGTAAGTCT 2252
 Db 1567 GTGACAAATGCTGTGAGCACTCTGAATGTGTGGAGAGAGGCTGTGTGAGGTAAGTCT 1626
 QY 2253 ATGTACAAACTTGTGTTTAAATCTGAGTTTGAAGTCAACCTTGAAGTATACGCCCTGAG 2312
 Db 1627 ATGTACAAACTTGTGTTTAAATCTGAGTTTGAAGTCAACCTTGAAGTATACGCCCTGAG 1686
 QY 2313 GCTAGTATGCTGTGATTTATGAAGACAAACAGTTACAGACAAATATGATGGGACT 2372
 Db 1687 GCTAGTATGCTGTGATTTATGAAGACAAACAGTTACAGACAAATATGATGGGACT 1746
 QY 2373 ACATTTGGGATATACCAAAAGCTGGTAAATGATATATCATGAGAAACACGCACTTGGCC 2432

Db 1747 ACATTTGGGATATACCAAAAGCTGGGTAATGATATATCATGAGAACACGCACTTGGCC 1806
 QY 2433 ATGAGTAATACGGCACTTCCCTGTACAGCTGTCTGTACAGTTGGGCTGTGACTG 2492
 Db 1807 ATGAGTAATACGGCACTTCCCTGTACAGCTGTCTGTACAGTTGGGCTGTGACTG 1866
 QY 2493 CCATGCTCTATGCTGTACAGCTGTACCGTTTGTGATATTTATCTGTTAATGATATC 2552
 Db 1867 CCATGCTCTATGCTGTACAGCTGTACCGTTTGTGATATTTATCTGTTAATGATATC 1926
 QY 2553 CGTTTGGGAAGCTCTCAAAAAAAAAAAAAAAAAAAAAA 2589
 Db 1927 CGTTTGGGAAGCTCTCAAAAAAAAAAAAAAAAAAAAAA 1963

RESULT 3
 AA87757
 ID AA87757 standard; cDNA; 1701 BP.
 AC
 XX
 AC
 XX
 AA87757;
 DT 28-NOV-2000 (first entry)
 XX
 XX
 DE Human secreted protein encoding cDNA SEQ ID #56.
 KW Human; secreted protein; forensic procedure; gene therapy;
 KW chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;
 KW cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
 KW brain disorder; skeletal muscle disorder; eye disorder; obesity;
 KW mitochondrial cyopathy; diabetes; atherosclerosis; Alzheimer's disease;
 KW neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
 KW septic shock; impotence; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200037491-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 20-DEC-1999; 99WO-1B02058.
 XX
 PR 22-DEC-1998; 98US-0113686.
 PR 25-JUN-1999; 99US-0141032.
 XX
 PA (GEST) GENSET.
 XX
 PI Bougueleret L, Dumas J, Duclert A;
 DR MPI; 2000-442637/38.
 DR P-PSDB; AAB25795.
 XX
 PT Polynucleotides and polypeptides encoding proteins with signal
 PT peptides, useful in diagnostic, forensic, gene therapy and chromosome
 PT mapping procedures.
 XX
 PS Claim 1, Page 221-223; 306pp; English.
 XX
 CC This sequence represents human cDNA encoding a secreted protein. The
 CC invention relates to sequences AA87725-A87774 which encode human
 CC secreted proteins AAB25763-B25812. The proteins include signal peptides.
 CC included in the invention are a host cell containing one of the cDNA
 CC sequences, and a purified antibody capable of binding to one of the
 CC secreted proteins. Also contained in the invention are methods for
 CC storing the sequence data on a computer system, and a method for
 CC identifying features of the cDNA sequences using a computer programme.
 CC The cDNAs are useful for expressing secreted proteins or fragments to
 CC obtain antibodies capable of specifically binding to the secreted
 CC proteins. The cDNAs may also be useful in diagnostic, forensic, gene
 CC therapy and chromosome mapping procedures and may be used to design
 CC expression vectors and secretion vectors. The proteins of the invention
 CC may be used to treat diseases including cancer, autoimmune diseases,
 CC cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological


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QY 1293 TTGGGGTTTCTAGAGTCGTG-----AGATAAATGATGAGACGCTGTAGCC 1343
DB 542 ATCCGGTTTCTCAGGTGTGTGAGCCACACAGAAAGAAACAAAGCGAGCTTCAAGTGTG 601
QY 1344 ATCCCGGTGATGAGAGAGTGAAGTGGGTGGTTCAGCTGACCCCTATTATTACATACC 1403
DB 602 ATTCAGTACGTGGGAGATGAGAGGTGCTACGGTGCAGCTGACCTCCATATTTTCTACT 661
QY 1404 TGCGCAATGATGATCTCCGACGAGGAGAGTGTGCTTTGCTGAGAGACAAGTGT 1463
DB 662 TGTGGCAGCGATGCTGATCCGACATTAAGAGAACATTTGCTGCTGCCCAAAAGGGCTC 721
QY 1464 CCATCCCTCCAGATGACACAGACGATGCTGGAGGCTGGCTCTCTTCCTGGTG 1523
DB 722 CCTTCCCTCTGATTAACAACAAAGCAAGCCGGAGGCTGGCTGCTCTCTCTCTGCTG 781
QY 1524 ---CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1580
DB 782 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 841
QY 1581 AGGAGCAGAGAGATGCTCTTCTATTTCCACATGCTCTGCCCCCTCATTAAGTCTCTG 1640
DB 842 AGATACAGAGAGATCTCTTTTCTA---CCACCACTACTGCCCCCATTAAGTCTCT 898
QY 1641 GTGTGTATCTCTGTGAGATATGTTTCATGACACCGTGTGTGCTTCACTACTCTTCT 1700
DB 899 GTGTGTATCCCATCTGAATATGTTTCATGACACCAATTTGTATCTTCACTGAATTTCT 958
QY 1701 CAAATCTACTGAGAGAGTGTATCTTGTGAAAATGCGAGAAAAGAAAATGCGAG 1760
DB 959 CAAATCTACTGAGAGAGTGTATCTTGTGAAAATGCGAGAAAAGAAAATGCGAG 1018
QY 1761 ATGGGGCCGGATGAGTGTGATGACCACTCAGAGCAGAGGAGATTAAGTGTCTTCTCT 1820
DB 1019 ATGGGTTCAGTGTGATGCTGTGCTTGCATCAAAAGAGAGAGCAAAAGTGTCTTCTCT 1078
QY 1821 CTTCCTCAGTGTGATGCTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTG 1880
DB 1079 CTTCCTCAGTGTGATGCTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTG 1138
QY 1881 AGGAGAACTCTCAGAGTGTGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1940
DB 1139 AGTGTGAACTCTCAGAGTGTGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1198
QY 1941 AGCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2000
DB 1199 AGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1258
QY 2001 GACTAATATGCTGTGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2060
DB 1259 GATTACATGCTGTGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1318
QY 2061 CACACAAATCTCTCAGAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2120
DB 1319 TGTGTGAACTCTCTCAGAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1378
QY 2121 CATGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2178
DB 1379 CAGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1438
QY 2179 TACTCTCTCTCTCAGAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2220
DB 1439 TATCTCAGCAATTAACAGGAGAAAACGTTGATGATCTCTGA 1480

```

RESULT 5
 AAS18126
 ID AAS18126 standard; cDNA; 1796 BP.
 AC
 XX AAS18126;
 XX
 DT 26-MAR-2002 (first entry)
 XX

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DE Human DNAX cytokine receptor subunit 6 (DCRS6) cDNA.
XX
KM Human: DNAX cytokine receptor subunit 6; DCRS6; phosphate labelling; ss;
KW gene therapy; protein therapy; immunological disorder.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 4..1512
FT /tag= a
FT /product= "Human DCRS6"
XX
PN WO200190358-A2.
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US16767.
XX
PR 24-MAY-2000; 2000US-206862P.
XX
PA (SCHE ) SCHERING CORP.
PI Gorman DM;
XX
XX MPI; 2002-106198/14.
XX DR P-PSDB; AUI1351.
XX
XX
PT Isolated antigenic human or mouse DNAX receptor subunit-like
PT polypeptide useful for detecting antibodies generated in response to
PT presence of increased protein levels or immunological disorders -
XX
PS Disclosure; Page 7-10; 148bp; English.
XX
CC The invention relates to primate and rodent DNAX cytokine receptor
CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
CC receptors, or their portions may be useful as phosphate labelling enzymes
CC to label general or specific substrates. The subunits may also be
CC functional immunogens to elicit recognising antibodies, or antigens
CC capable of binding antibodies. A combination, e.g., including a DCRS can
CC be used as an immunogen for the production of antisera or antibodies
CC capable of distinguishing between other cytokine receptor family members.
CC A purified DCRS can also be used as a reagent to detect antibodies
CC generated in response to the presence of elevated levels of expression,
CC or immunological disorders which lead to antibody production to the
CC endogenous receptor. This sequence represents cDNA encoding the human
CC DCRS6 polypeptide.
XX
SQ Sequence 1796 BP; 514 A; 439 C; 399 G; 444 T; 0 other;
XX
Query Match 24.9%; Score 644.8; DB 24; Length 1796;
Best Local Similarity 76.0%; Pred. No. 5.5e-182;
Matches 853; Conservative 0; Mismatches 252; Indels 17; Gaps 4;

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QY 1404 TGGGCAATGACTGATCCGACGCGAAGGACAGTTGCTTGTCTCAGACAACTGCT 1463
 XX |||||
 OS 772 TGTGGAGGAGACTGATCCGACATTAAGGAACAGTTGTGCTCTGCCACAAACAGCGCTC 831
 QY 1464 CCCATCCCTCCAGATGACAAACAGCCATGCTGGAGGCGTGGCTCTCTCCCTGGG 1523
 DB 832 CCTTCCCTCTGGATTAACAACAAAGCAGGCGGGAGGCTGGCTCTCTCTCTGGCTG 891
 QY 1524 ---CTGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1580
 DB 892 TCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 951
 QY 1581 AGGAGACGAGAGAGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1640
 DB 952 AGGATCAAGAGAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1008
 QY 1641 GGGGTTATCTCTGAGATATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1700
 DB 1009 GTGGTTTACCATCTGATAATATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1068
 QY 1701 CAAACTACTGACAGAGTGAAGTCACTCTTGAATAAATGGAGAAATAATCGCGAG 1760
 DB 1069 CAAACCATTTGACAGAGTGAAGTCACTCTTGAATAAATGGAGAAATAATGAGAG 1128
 QY 1761 ATGGGCGCGTGAAGTGGCTGACCACTCAGAACAGCGGACAGATAAGTGTCTTCTT 1820
 DB 1129 ATGGGCGCGTGAAGTGGCTGACCACTCAGAACAGCGGACAGATAAGTGTCTTCTT 1188
 QY 1821 CTTCCTGAGAGTCCCGACCTTCTTGTGACAGTCTGCTGGCCCAATAGAGGCGAGCGC 1880
 DB 1189 CTTCCTGAGAGTCCCGACCTTCTTGTGACAGTCTGCTGGCCCAATAGAGGCGAGCGC 1248
 QY 1881 AGGAGAACTCTCAGAGTCTGTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1940
 DB 1249 AGTGAAGACTCTCAGAGTCTGTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1308
 QY 1941 AGCCAGACGCTATGACAAATATCTGTTGTCTTCTTCTTCTTCTTCTTCTTCTTCT 2000
 DB 1309 AGCCAGATTCATCTGACAAATATCTGTTGTCTTCTTCTTCTTCTTCTTCTTCTTCT 1368
 QY 2001 GACTATATGCTCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2060
 DB 1369 GATTATATGCTCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1428
 QY 2061 CACACGAATCTCTCAAGGCTACGAGAGAGTCACTGTAAGAAAGCTCACAAGCTGCTG 2120
 DB 1429 TGTGCAAACTTCTCATGTCAAGAGAGTCTGAGCAAGAAAGATCAAGCTTCTG 1488
 QY 2121 CATGATAGCTGTTCACTTGTAGTCACTGAGGAGGAA--TGAAGACTGTAAGCTTCTG 2178
 DB 1489 CAGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1548
 QY 2179 TACTCTCCCTTCCAGTGAATAATGCTGTGTGACGACTCTGAA 2220
 DB 1549 TATCCCAACCAATTACAGGGAATAAAGTGTGATGATCTGAA 1590
 RESULT 6
 AAD12581
 ID AAD12581 standard; cDNA; 1818 BP.
 AC AAD12581;
 XX
 XX 25-SEP-2001 (first entry)
 XX
 DE Human protein having hydrophobic domain encoding cDNA clone HP10758.
 XX
 XX Human; hydrophobic domain; gene therapy; nutritional supplement;
 KM cell proliferation; immunomodulatory; autoimmune disorder; antidiabetic;
 KM multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
 KM haematopoiesis; tissue growth activity; Parkinson's disease; cystostatic;
 KM Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
 KM haemostatic; thrombolytic; tumour growth inhibitor; anabolic;

KW contraceptive; antifertility; antiinflammatory; ss.
 XX Homo sapiens.
 OS
 XX
 PH Key Location/Qualifiers
 FT CDS 26..1534
 FT /tag= a
 FT /product= "Human protein having hydrophobic domain"
 FT /note= "CDS is specifically claimed in claim 3"
 FT sig_peptide 26..70
 FT /tag= b
 FT mat_peptide 71..1531
 FT /tag= c
 FT /product= "Mature human protein with hydrophobic domain"
 PN MO200149728-A2.
 PD 12-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-JP09359.
 PR 06-JAN-2000; 2000JP-0000585.
 PR 06-JAN-2000; 2000JP-0000588.
 PR 11-JAN-2000; 2000JP-0002299.
 PR 03-FEB-2000; 2000JP-0026862.
 PR 03-MAR-2000; 2000JP-0058367.
 XX
 PA (PROT-) PROTEGENE INC.
 PA (SAGA) SAGAMI CHEM RES CENT.
 PI Kato S, Kimura T;
 XX
 DR WPI; 2001-418355/44.
 DR P-PSDB; AAE06586.
 XX
 PT Human proteins with hydrophobic domains and the nucleic acids encoding
 PT them, useful for preventing diagnosing and treating e.g. cancer,
 PT Alzheimer's and inflammation -
 PT
 PS Claim 4; Page 340-344; 563pp; English.
 XX
 CC The present sequence is human protein with hydrophobic domain encoding
 CC cDNA clone HP10758. The polynucleotide and polypeptide of the invention
 CC may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The polynucleotides
 CC may be used to produce the polypeptide, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the protein. The
 CC polynucleotides and its complementary sequences may also be used as DNA
 CC probes in diagnostic assays and also used in gene therapy. The
 CC polypeptides may also be used as antigens in the production of antibodies
 CC and in assays to identify modulators of polypeptide expression and
 CC activity. The polypeptides and nucleic acids may be used as nutritional
 CC supplements, to modulate cytokine and cell proliferation activity, to
 CC modulate immune stimulation or suppression (e.g. for the treatment of
 CC microbial infections and autoimmune disorders such as multiple sclerosis,
 CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
 CC haematopoiesis, to modulate tissue growth activity (e.g. for the
 CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
 CC disease), to modulate activin and inhibin activity (e.g. for controlling
 CC fertility), to modulate chemotactic and chemokinetic activity, to
 CC modulate haemostatic and thrombolytic activity, to modulate receptor
 CC ligand activity, to modulate inflammation and to inhibit tumour growth.
 CC
 SQ Sequence 1818 BP; 522 A; 447 C; 404 G; 445 T; 0 other;

Query Match 24.9%; Score 644.8; DB 22; Length 1818;
 Best Local Similarity 76.0%; Pred. No. 5,5e-182;
 Matches 853; Conservative 0; Mismatches 252; Indels 17; Gaps 4;

QY 1113 TTCACATTCACGAGCTGCTTAACACGTAATATTAATAAGACGTGACATGAGGG 1172
 DB 494 TTCACCTACCGAGCTGCTTAACACCAATATTAATAAAGGTGTCAAGGCC 553


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QY 1173 GGAAGCTGTGGAGCCAGACATCACTGCTTTGTAAGAAAGAAAGAAAGATGGTTGAAGTG 1232
DB 554 GGAAGCTGTGGAGATCCGAACATCACTGCTTTGTAAGAAAGAAAGATGAAGAGACGTAGAAAGTG 613
QY 1233 AATTTCACAAACCATTCCTCTTGGAAACAGATACAGATTCATTCATTTCAACGGGACACGACA 1292
DB 614 AACTTCACAAACCACTCTCTCTGGGAAACAGATACATGGCTCTTATTCACACACAGCATATC 673
QY 1293 TTGGGGTTTTCTAGAGTCTGG-----AGATAAACTGATGAGAGAGCTGTGAAGC 1343
DB 674 ATCGGGTTTTCTAGAGTGTGTTGAGCCACACAGAAAGAAACAAACGACAGCTTCAAGTGTG 733
QY 1344 ATCCGGTGACTGAGAGAGTGAAGGTGGCGGTGTGCTGACCTGACCCCATATTTACATACC 1403
DB 734 ATTCAGATGACTGGGAGTAGTGAAGGTGTACGGTGCAGCTGATCCATATTTTCTACT 793
QY 1404 TGGGGCAATGATGCAATCCACCGGAAAGGACAGTTGTGCTTTGCTAGAGACAAAGTGT 1463
DB 794 TGTGGCAGCAGTGCATCCGACATAAAGAAACAGTTGTGCTGTGCGACAAACAGCGCTC 853
QY 1464 CCATCCCTCAGATGACAAACAGACGATGTGGAGAGTGGCTGTGCTCTTCTGTGTG 1523
DB 854 CTTTCCCTCTGATTAACAAACAAAGCAGACCGGAGGCTGTGCTCTCTCTCTGTG 913
QY 1524 ---CTGCTGTGTGTGTGTGGGTGTGGCAGCTGGATCTACTACTTGGAGGCAAGAA 1580
DB 914 TCTCTGTGTGTGTGTGTGGGTGTGGCAGGATCTATCTATGTGAGGACGAA 973
QY 1581 AGAGAGCAGAAAGCTCTTCTTCCATTTTCCACCAATGCTCTGCGCCCTCATTAAGTCTTG 1640
DB 974 AGGATCAAGAAAGACTCTCTTTCTA---CAACACACTACTGCCCCCATTAAGTCTT 1030
QY 1641 GTGGTTATCTCTGAGATATGTTTCATACACACCGCTGTGCTTCACTGACTTTCTT 1700
DB 1031 GTGGTTATCCCATGTGAATATGTTTCATACACATTTGTTACTTCACTGAAATTTCTT 1090
QY 1701 CAAAACCTACTGACAGAGTGAAGTCACTCTTGAAGAAATGGCAAGAAAGAAATGCGGAG 1760
DB 1091 CAAAACCTACTGACAGAGTGAAGTCACTCTTGAAGAAATGGCAAGAAAGAAATGCGGAG 1150
QY 1761 ATGGGCGCGGTACAGTGTGTGACCTACACAGAAACCGGCAAGTAAAGTGTCTTCTT 1820
DB 1151 ATGGGTCAAGTGAAGTGTGTGACCTACACAAAGAAAGCAGACAAAGTGTCTTCTT 1210
QY 1821 CTTCCAGTACGTCGCCAGCCCTTTTGTGACAGTGTCTGTGGCCCAATGAGGAGCGGCC 1880
DB 1211 CTTTCCAGTACGTCGAACAGTGTGTGAGTGTACCTGTGGCAAGAGCGAGGGCAGTCCC 1270
QY 1881 AGGAGAACTCTCAGAGTGTGTGCTCTTCTTAACTCTTTTGTAGTGAATTCAGC 1940
DB 1271 AGTGAAGAACTCTCAGAGCTCTTCTCTGCTTTAACTCTTCTGCAGTGAATCTAAGA 1330
QY 1941 AGCAGACGATCTGCAACAAATCTGTGTGTCTATCTTGGGGGAGAGACCTCAAGGC 2000
DB 1331 AGCAGATTTATCTGCAAAATAGTGTGTCTACTTAAAGAGATTGATACAAAGAC 1390
QY 2001 GACTATATCTCCGAGTGTCTGCCCCCAATATCATCTCATGAAGAGCGCAGAGCTTTC 2060
DB 1391 GATTACATGCTCTCAGTGTCTGCCCCAATACCACTCATGAAGATGCACTGCTTTC 1450
QY 2061 CACACAGAACTTCTCAGGCTTACGAGAGATGTCAGTGAAGAAACGCTCAACAGCTGC 2120
DB 1451 TGTGCAAGAACTTCTCTCATGTCTCAAGCAGCAGTGTCAAGAAAGATCAAGCTGC 1510
QY 2121 CAGTATGCTGTTCACCTTGTAGTCAACCGGGGAA--TAAGACTCTGAAGCTTTC 2178
DB 1511 CAGATGTGCTGTCTCTTGTAGCCCAACCATGAGAAAGAGAGACTTAAAGGCTTTC 1570
QY 2179 TACTCTCCCTTCAGTGAAGAAATGCTGTGAGAGACTTGAA 2220
DB 1571 TATCCACCAATTAAGAGGAAAGAAAGTGTGATGATCTTGA 1612

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RESULT 7
AAH99008
ID AAH99008 standard; cDNA; 2161 BP.
XX
AC AAH99008;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 865.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN MO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001MCO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617446.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSF-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
XX
PT P-PSDB; AAM24349.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX
PS Claim 1; Page 707; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX from the organism of interest. They can be used in diagnostics,
XX forensics, gene mapping, identification of mutations, to assess
XX biodiversity and for nutritional purposes. The present sequence is a cDNA
XX of the invention.
SQ Sequence 2161 BP; 639 A; 516 C; 446 G; 560 T; 0 other;

Query Match 24.9%; Score 644.8; DB 22; Length 2161;
Best Local Similarity 76.0%; Pred. No. 6; 1e-182; Indels 17; Gaps 4;
Matches 853; Conservative 0; Mismatches 252;

QY 1113 TTCACATTCCTCCAGGCTGCTTAACACAGTAATGAATTAAGACAGTGCATGAGCG 1172
DB 476 TTCACCTACACAGGCTGCTTAACACAGTAATGAATTAAGAAAGTGTCAAGGCC 535
QY 1173 GGAAGCTGTGGAGCCAGACATCACTGCTTTGTAAGAAAGAAAGATGGTTGAAGTG 1232
DB 536 GGAAGCTGTGGAGATCCGAACATCACTGCTTTGTAAGAAAGATGAGAGACAGTGAAGTG 595
QY 1233 AATTTCACAAACCATTCCTCTTGGAAACAGATACAGATTCATTCACCGGACACAGACA 1292
DB 596 AACTTCACAAACCACTCTCTGGGAAACAGATACAGGCTCTTATCCACACAGCACTATC 655
QY 1293 TTGGGGTTTTCTAGAGTCTGG-----AGATAAACTGATGAGAGCGTGTAGCC 1343
DB 656 ATCGGGTTTTCTCAGTGTGTTTGAAGCAGACAGAAAGAAACAAACGAGCTTCAAGTGTG 715
QY 1344 ATCCGGTGACTGAGAGAGTGAAGGTGGGTGTTCAAGCTGACCCCATATTTACATACC 1403

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Db 716 ATTCGAGTCTGGGATATGAAAGGTGACGCTGACGTGATCCATATTTTCTACT 775
1404 TGGGGAATAGCTGATCCGACCGGAAGGACAGTTGTGCTTTGCTCAGACAAAGTCT 1463
776 TGTGGACGACATGATCCGACATAAAGGAACATTTGTGCTGCTCCACAAAGGCTC 835
1464 CCCATCCTTCAGATGACAAAGAGCATGCTGGAGAGCTGCTGCTCTCTTCTGCTG 1523
836 CTTTCCCTCTGATTAACAACAAAGCAAGCCGGAAGCTGGCTGCTCTCTCTGCTG 895
1524 ---CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1580
896 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 955
1581 AGGAGACGAAAGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1640
956 AGGATCAAGAAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1012
1641 GTGGTTATCTCTGATGATATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1700
1013 GTGGTTATCCCATCTGAAATATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1072
1701 CAAACCTACTGCAAGAGTGAAGTCTTGAATAATGCAAAAGAAATGCGCGAG 1760
1073 CAAACCTACTGCAAGAGTGAAGTCTTGAATAATGCAAAAGAAATGCAAGAG 1132
1761 ATGGGGCCGGTACAGTGGCTGACCATCTGACAGCAAGCGGCAATTAAGGTCTT 1820
1133 ATGGGTCAGAGTGAAGTGGCTTGGCCATCAAAAGAGCAAGCAAGTCTTCTT 1192
1821 CTTCCTGAGTGAAGTGGCGACCTTTGTCAGTGTGCTGCTGCTGCTGCTGCTG 1880
1193 CTTCCTGAGTGAAGTGGCGACCTTTGTCAGTGTGCTGCTGCTGCTGCTGCTG 1252
1881 AGGAGAACTCTGAGAGTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1940
1253 AGGAGAACTCTGAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1312
1941 AGGAGAACTCTGAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2000
1313 AGGAGAACTCTGAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1372
2001 GACTATATGCTCTGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2060
1373 GATTACAAATGCTCTGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1432
2061 CACACAACTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTG 2120
1433 TGTGCAAGCTCTGATGTCAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1492
2121 CATGATAGCTGCTTACCTCTGATGTCAGAGAGTGTGAGAGAGTGTGAGAGAG 2178
1493 CAGGATAGCTGCTTCTGATGTCAGAGAGTGTGAGAGAGTGTGAGAGAGTGTG 1552
2179 TACTCTCTCTGAGTGAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 2220
1553 TATCCACCAATTAACAGGAAAAAAGTGTGATGATCTTGA 1594

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KW interleukin 17; immune system disorder; infection; weight; reproductive;
KW neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation;
KW glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;
KW tumour; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 273..1430
FT /tag=a
FT /product="Human IL-17 receptor-like protein #3"
PN WO200168705-A2.
PD 20-SEP-2001.
PP 16-MAR-2001; 2001WO-US08688.
PR 16-MAR-2000; 2000US-189923P.
PR 12-MAY-2000; 2000US-204208P.
PR 27-NOV-2000; 2000US-0723232.
PR 02-FEB-2001; 2001US-266159P.
XX (AMGE-) AMGEN INC.
PI Jing S, Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ,
DR MPI: 2002-055100/07.
DR P-PSDB; AAM47459.
XX
PT Three human nucleic acids encoding interleukin 17 (IL-17) receptor like
PT polypeptides, useful for treating, diagnosing, ameliorating or
PT preventing immune system disorders (e.g. psoriatic arthritis) and
PT infections (e.g. viral infections) -
XX
XX Claim 1; Fig 5; 239p; English.
XX
XX The present invention relates to novel human nucleic acids encoding
XX interleukin 17 (IL-17) receptor like proteins. The present sequence is
XX one such coding sequence. The IL-17 receptor-like proteins and coding
XX sequences are useful for treating a pathological condition related to
XX immune system dysfunction (e.g. psoriatic arthritis), infections (e.g.
XX viral infections), weight disorders (e.g. obesity), neuronal dysfunction
XX disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin
XX disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis),
XX bone disease (e.g. osteoporosis), vascular system disorders (e.g.
XX ischaemia), eye disorders, reproductive disorders, tumours and
XX inflammation.
XX
SQ Sequence 1713 BP; 488 A; 419 C; 385 G; 421 T; 0 other;

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Query Match 24.8%; Score 643.2; DB 24; Length 1713;
Best Local Similarity 75.9%; Pred. No. 1.6e-181;
Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;

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QY 1113 TTCACATTCGCGGCTGCTTAACCAACGTAATGAATATATAAAGCAGTGAAGCG 1172
Db 390 TTCACCTCACAGGCTGCTTAACCAACGTAATGAATATATAAAGTGTGCAAGGCC 449
QY 1173 GGAAGCTGTGGAGCCGACACATCACTGCTTGTAAAGAAAGAGAGTGTGAAGTG 1232
Db 450 GGAAGCTGTGGAGATCCGAACATCACTGCTTGTAAAGAAAGAGAGAGTGTGAAGTG 509
QY 1233 AATTTCACAAACCAATCCCTTGGAAACATACAGATTCTCATTTAAGGGACACAGACA 1292
Db 510 AACTTCACAAACCACTCCCTGGAAACAGATACATGCTTATCCAAACAGCACTATTC 569
QY 1293 TTGGGGTTTCTAGAGTGTGCTG-----AGAAATAACTGATGAGAGCTGTGAAGCC 1343
Db 570 ATCGGGTTTCTCAGGTGTTTGAAGCCACACAGAAAGAAACAAAGCACTTCAAGTGTG 629
QY 1344 ATCCCGGTGCTGAGAGAGTGAAGGTGGGTGTTCACTGACCTGACCCCATATTTTACATACC 1403

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RESULT 8
ABR03202
ID ABR03202 standard; cDNA; 1713 BP.
AC ABR03202;
XX
XX
XX 11-FEB-2002 (first entry)
DE Human IL-17 receptor like protein #3 coding sequence.
XX
XX Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic;
KW antiproliferic; antimicrobial; anorectic; neuroprotective;
KW antiallergic; dermatological; cyostatic; gene therapy;

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Db 630 ATTCAAGTACTGGGGATAGTGAAGTGTCTACGGTGCAGCTGACTCCATATTTTCTACT 689
Qy 1404 TGGCGCAATGATCTGCATCCGACGCGAAGGGAACAATTGCTTTGCTTCAGAGCAAGTGTCT 1463
Db 690 TGTGGACGCGATCTGCATCCGACATTAAGGAACAGTTGGCTCTGCTCCCAACAGAGGCTC 749
Qy 1464 CCGATCCCTCCAGATGACACAGACAGATGCTGGAGGCTGGCTGCTCTCTTCCTGGTG 1533
Db 750 CTTTCCCTCTGAGTAAACAAAGCAAGAGCGGAGGCTGGCTGCTCTCTCTGCTG 809
Qy 1524 ---CTGGGAGGCTGTGTGGGTGTGGGAGCTGGGAGCTGACCTTAACCTTGGAGGCAAGGA 1580
Db 810 TCTCTGGTGGGCGACATGGGTGTGGGAGGATCTATCTTAAGTGGAGCGAAG 869
Qy 1581 AGGAGCAGAGAGAGCTCTTCTATTTTCCACCATGCTCTGCCCCCTCATTAAGTGTCTG 1640
Db 870 AGGATCAAGAGAGCTCTTCTTTTA---CCACCACTACTGCCCCCATTAAGTGTCTT 926
Qy 1641 GTGGTTATCTCTTGAGATATGTTTCCATGACACCGCTGTGCTGCTTCACTGACTTTCTT 1700
Db 927 GTGGTTTACCATCTGAAATATGTTTCCATCACAATTTGTTCACTGAATTTCTT 986
Qy 1701 CAAATCTACGAGAGAGAGTATCTCTTGAATAATGGAGAGAGAGAGAGAGAGAGAGAG 1760
Db 987 CAAATCAATGACAGAGAGTATCTCTGAAAAAGTGGAGAGAGAGAGAGAGAGAGAGAG 1046
Qy 1761 ATGGGGCCGGATGACAGTGTGACCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1820
Db 1047 ATGGGTTCAGTGCAGTGTGCTTGCATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1106
Qy 1821 CTTTCCAGTGCAGTGTGCGAGCCCTTTGTGACAGTGTGCTGTGGCAATGAGGAGAGAG 1880
Db 1107 CTTTCCAGTGCAGTGTGCGAGAGTGTGCGATGTACTGTGGCAAGAGAGAGAGAGAGAG 1166
Qy 1881 AGGAGAGAGTCTGAGAGTGTGCTCTTGGCTTGAACCTTTTGAAGATTTGACG 1940
Db 1167 AGTGAAGTCTTCAAGAGCTCTTCCCTTGGCTTTAACTTTTCTGAGTGTAAAGA 1226
Qy 1941 AGCAGAGAGTCTGACAAATACCTGGTGTCTATCTTGGGGAGAGAGAGAGAGAGAGAG 2000
Db 1227 AGCCAGTTTCACTGCAAAATAGTGTGTCTACTTTGAGAGATGATTAACAAAGAG 1286
Qy 2001 GACTATATGCTCTGAGTGTGCTGCCCCCAATATATCTCATGAGAGAGAGAGAGAGAG 2060
Db 1287 GATTACATGCTCTCAGTGTCTGCCCCCAAGTACCACTCATGAGAGAGAGAGAGAGAG 1346
Qy 2061 CACAGAGAGTCTCTCAAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2120
Db 1347 TGTGCAAGAGTCTCTCAATGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1406
Qy 2121 CATGATAGTGTGTCACCTTGTATGTCACCGGGGAGAA--TAGAGACTGTGAAGCTTTC 2178
Db 1407 CAGATGTGCTGTGCTCTCTTGTAGCCCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1466
Qy 2179 TACTCTCCCTTCCAGTGAACAATGCTGTGAGCAGCTCTGAA 2220
Db 1467 TATGCCACCAATTAACAGGAGAAAAACGTGTGATGATCTGAA 1508

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RESULT 9
AADI3443
ID AADI3443 standard; cDNA; 1827 BP.

XX AADI3443;

DT 06-NOV-2001 (first entry)

DE Human interleukin-17 receptor related protein (Evi27) encoding cDNA #1.

KM Human interleukin-17 receptor related protein; IL-17; chromosome 3p21;

KW Evi27; retroviral integration; chromosomal mapping; mutational analysis;

KW BXH2 murine myeloid leukemia; proinflammatory cytokine; IL-8; therapy;

KW haematopoietic cell; cancer; autoimmune disease; ss.

```

XX OS Homo sapiens.
XX Key Location/Qualifiers
XX CDS 6..1514
FT sig_peptide /tag= a
FT /product= "Human Evi27 protein"
FT mat_peptide /tag= b
FT /product= "Human mature Evi27 protein"
XX MO200157202-A2.
XX 09-AUG-2001.
XX 02-FEB-2001; 2001WO-US03518.
XX 04-FEB-2000; 2000US-0180374.
XX (UYAR-) UNIV ARKANSAS.
XX Shaughnessy JD;
XX WPI; 2001-496920/54.
XX P-PSDB; AAE07160.
XX New nucleic acids encoding an interleukin (IL)-17 receptor related
XX protein for use as a marker for leukemia
XX Claim 1a; Page 74-75; 87bp; English.
XX
XX The present sequence is a cDNA encoding human interleukin (IL)-17
XX receptor related protein (Evi27). Human Evi27 gene was mapped to
XX chromosome 3p21. Evi27 is a common site of retroviral integration
XX in BXH2 murine myeloid leukemias. Evi27 cDNA sequences are useful
XX as antisense molecules to inhibit Evi27 protein or for chromosomal
XX mapping or mutational analysis of Evi27 protein. They are proviral
XX integration sites associated with leukemias and monitoring this
XX site provides a genetic tag for disease gene identification. The
XX proteins of the invention are useful to stimulate the secretion of
XX proinflammatory cytokines such as IL-8 and plays an important role
XX in the developmental and/or disease processes of haematopoietic
XX cells. Hence modulating the expression of Evi27 at the RNA or
XX protein level is used in the treatment of diseases such as cancer
XX or autoimmune diseases.
XX
XX Sequence 1827 BP; 547 A; 438 C; 397 G; 445 T; 0 other;
XX
XX Query Match 24.8%; Score 643.2; DB 22; Length 1827;
XX Best Local Similarity 75.9%; Pred. No. 1.7e-181;
XX Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;

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 DB 954 AGGATCAAGAAAGACTTCTTTCTTA---CCACCACACTACTGTGCCCCCATTAAGTCTCT 1010
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 QY 1881 AGGAGAGTCTGAGAGTGTGCTGCTTGAACCTCTTGTGATGATTTCAAG 1940
 DB 1251 AGTGAAGTCTTGAAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1310
 QY 1941 AGGCAAGTCTGAGAGTGTGCTGCTTGAACCTCTTGTGATGATTTCAAG 2000
 DB 1311 AGGCAATTCATCTGAGAGTGTGCTGCTTGAACCTCTTGTGATGATTTCAAG 1370
 QY 2001 GACTATTAATGCTGAGTGTGCTGCTTGAACCTCTTGTGATGATTTCAAG 2060
 DB 1371 GATTAAAGTCTGAGTGTGCTGCTTGAACCTCTTGTGATGATTTCAAG 1430
 QY 2061 CACAGAGTCTGAGAGTGTGCTGCTTGAACCTCTTGTGATGATTTCAAG 2120
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 DB 1491 CAGGATAGTCTGAGAGTGTGCTGCTTGAACCTCTTGTGATGATTTCAAG 1550
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 ID AAD28776 standard; DNA; 1841 BP.
 AC AAD28776;
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 XX
 DT 07-MAY-2002 (first entry)
 DE Human Interleukin-17 receptor B-2 (IL-17RB-2) DNA.
 KW Human; interleukin-17 receptor B-2; IL-17RB-2; immune system dysfunction;
 KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;
 KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;
 KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;
 KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;

KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;
 KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;
 KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;
 KW cancer; diabetes; ds.
 OS Homo sapiens.
 XX
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 FT Key Location/Qualifiers
 FT CDS 50..1558
 FT /tag= a
 FT /product= "Human IL-17RB-2 protein"
 FT sig_peptide 50..92
 FT /tag= b
 FT mat_peptide 93..1555
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 FT /product= "Mature IL-17RB-2 protein"
 PN WO200208285-A2.
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 PD 31-JAN-2002.
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 PF 21-JUN-2001; 2001MO-US19861.
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 PR 22-JUN-2000; 2000US-213125P.
 PR 02-FEB-2001; 2001US-266159P.
 PR 16-MAR-2001; 2001US-0810384.
 PA (AMGE-) AMGEN INC.
 XX
 PI Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;
 DR WPI: 2002-155217/20.
 XX
 PT P-PSDB: AAE18127.
 XX
 PT Nucleic acid molecules encoding Interleukin 17 (IL-17) - like
 PT polypeptides useful in the treatment, prevention and diagnosis of
 PT diseases e.g. cancer -
 XX
 PS Disclosure: Page 230-232; 242pp; English.
 XX
 CC The invention relates to nucleic acid molecules encoding Interleukin 17
 CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels
 CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,
 CC preventing or ameliorating a disease, such as immune system dysfunction
 CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease);
 CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel
 CC disease, transplant rejection, graft vs. host disease); infections (HIV,
 CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,
 CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung
 CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin
 CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone
 CC (osteoporosis); Paget's disease; hypercalcaemia) vascular system (epilepsy
 CC atherosclerosis, heart failure, angiogenesis); tumour, cancers (lymphoma
 CC leukaemia); reproductive (infertility, miscarriage, endometriosis); eye
 CC (blindness, retinal neuropathy) and treatment of diseases involving
 CC inflammation. The present sequence is human Interleukin-17 receptor B-2
 CC (IL-17RB-2) DNA.
 CC
 XX
 SQ Sequence 1841 BP; 522 A; 455 C; 416 G; 448 T; 0 other;
 XX
 Query Match 24.8%; Score 643.2; DB 24; Length 1841;
 Best Local Similarity 75.9%; Pred. No. 1.7e-181;
 Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;
 QY 1113 TTCACATTCGAGGCTGCTTAACCAAGTAATGAATATAAAGACGCTGAGGCG 1172
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 QY 1173 GGAAGCTGTGGAGCCGACATCTGCTTTAAAGAAAGAGAGATGTTGAAGTG 1232
 DB 578 GGAAGCTGTGGATTCGAAATCTACTGCTTTAAAGAAAGAGAGACAGTGAAGTG 637

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RESULT 11
ABR03200
ID ABA03200 standard; cDNA; 1841 BP.
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AC ABA03200;
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XX
XX 11-FEB-2002 (first entry)
DE Human IL-17 receptor like protein #1 coding sequence.
XX
XX Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic;
XX antiparasitic; antimicrobial; anorectic; neuroprotective;
XX antidiabetic; antiallergic; dermatological; cytostatic; gene therapy;
XX interleukin 17; immune system disorder; infection; weight; reproductive;
XX neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation;
XX glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;
XX tumour; ss.
XX
XX Homo sapiens.
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XX FT /product="Human IL-17 receptor-like protein #1"
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XX MO200168705-A2.
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XX PD 20-SEP-2001.
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XX PF 16-MAR-2001; 2001WO-US08688.
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XX PR 16-MAR-2000; 2000US-189923P.
XX PR 12-MAY-2000; 2000US-204208P.
XX PR 27-NOV-2000; 2000US-0723232.
XX PR 02-FEB-2001; 2001US-266159P.
XX
XX (AMGE-) AMGEN INC.
XX
XX PI Jing S, Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ.
XX
XX WPI; 2002-055100/07.
XX DR P-PSDB; AAM47456.
XX
XX PT Three human nucleic acids encoding interleukin 17 (IL-17) receptor like
XX PT polypeptides, useful for treating, diagnosing, ameliorating or
XX PT preventing immune system disorders (e.g. psoriatic arthritis) and
XX PT infections (e.g. viral infections).
XX
XX PT Claim 1; Fig 1; 239p; English.
XX
XX PS
XX CC The present invention relates to novel human nucleic acids encoding
XX CC interleukin 17 (IL-17) receptor like proteins. The present sequence is
XX CC one such coding sequence. The IL-17 receptor-like proteins and coding
XX CC sequences are useful for treating a pathological condition related to
XX CC immune system dysfunction (e.g. psoriatic arthritis), infections (e.g.
XX CC viral infections), weight disorders (e.g. obesity), neuronal dysfunction
XX CC disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin
XX CC disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis),
XX CC bone disease (e.g. osteoporosis), vascular system disorders (e.g.
XX CC ischaemia), eye disorders, reproductive disorders, tumours and
XX CC inflammation.
XX
XX SQ Sequence 1841 BP; 522 A; 455 C; 416 G; 448 T; 0 other;
XX
XX
XX Query Match 24.8%; Score 643.2; DB 24; Length 1841;
XX Best Local Similarity 75.9%; Pred. No. 1.7e-181;
XX Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;
XX
XX
XX 1113 TTCACTTCCCGGCTGCTTAACAGTAATATTAATAAGCAGTGCATGAGGC 1172
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XX 1173 GGAAGCTGTGGGACCCAGACATCACTGCTTGTAAAGAAAGAGAGATGTGTAAGT 1232
XX 578 GGAAGCTGTGGGATCCAGACATCACTGCTTGTAAAGAAAGAGAGACAGTGAAGT 637
XX
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Db 638 AACTTACAAACCACTCCCTGGGAAAAGATATCATGCTCTTATCCAAACACACACTATC 697
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 Db 818 TGGGAGGAGCACTGACATCCCACTAAAGAAAGATGTGTCTGCCCCAACAAGAGCGTC 877
 1464 CCCATCCCTCAGATGACAAAGAGCATGCTGGAGGCTGGGCTGCTCTTCTGCTG 1523
 Db 878 CTTTCCCTCTGATTAACAAACAAAGAGAGCGGAGGCTGGCTGCTCTCTCTGCTG 937
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 Db 1235 CTTTCAATGACGTCAACAGTGTGTGATGTGACCTGTGGCAAGAGCGAGGAGTCTCC 1294
 1881 AGGAGAACTCTGAGATCTGCTCTCTTCTTGAAGTCTTCTTGTAGTATTCAGC 1940
 Db 1295 AGTGAAGTCTCAAGACCTCTTCTTCTTGAAGTCTTCTTGTAGTATTCAGC 1354
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 2001 GACTAATAGCCCTGAGT 2060
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RESULT 12
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 ID AAD28777 standard; DNA; 2015.BP.
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 AC AAD28777;

XX 07-MAY-2002 (first entry)
 DT Human Interleukin-17 receptor B-3 (IL-17RB-3) DNA.
 DE Human, interleukin-17 receptor B-3; IL-17RB-3; immune system dysfunction;
 XX cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;
 KM inflammatory bowel disease; neuronal dysfunction; transplant rejection;
 KM autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;
 KM infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;
 KM cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;
 KM eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;
 KM epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;
 KM leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;
 KM cancer; diabetes; ds.
 XX Homo sapiens.
 OS
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 XX Key Location/Qualifiers
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 FT /product= "Human IL-17RB-3 protein"
 FT sig_peptide 50..92
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 FT mat_peptide 93..1729
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 XX
 XX WO200208285-A2.
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 XX 31-JAN-2002.
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 XX 21-JUN-2001; 2001WO-US19861.
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 XX 22-JUN-2000; 2000US-213125P.
 XX 02-FEB-2001; 2001US-266159P.
 XX 16-MAR-2001; 2001US-0810384.
 XX
 XX (AMGE) AMGEN INC.
 PA
 PI Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;
 DR WPI; 2002-155217/20.
 XX P-PSDB; AAE18128.
 XX
 XX Nucleic acid molecules encoding Interleukin 17 (IL-17) - like
 PT polypeptides useful in the treatment, prevention and diagnosis of
 PT diseases e.g. cancer
 PS
 XX Disclosure; Page 234-236; 242pp; English.
 XX
 CC The invention relates to nucleic acid molecules encoding Interleukin 17
 CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels
 CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,
 CC preventing or ameliorating a disease, such as immune system dysfunction
 CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease);
 CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel
 CC disease, transplant rejection, graft vs. host disease); infections (HIV,
 CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,
 CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung
 CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin
 CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone
 CC (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy
 CC atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma
 CC leukaemia); reproductive (infertility, miscarriage, endometriosis); eye
 CC (blindness, retinal neuropathy) and treatment of diseases involving
 CC inflammation. The present sequence is human Interleukin-17 receptor B-3
 CC (IL-17RB-3) DNA.
 XX
 XX Sequence 2015 BP; 541 A; 499 C; 475 G; 500 T; 0 other;
 XX
 XX Query Match 24.8%; Score 643.2; DB 24; Length 2015;
 XX Best Local Similarity 75.9%; Pred. No. 1.8e-181;

Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;

QY 1113 TTCACTTCCAGGCTGCTTAAACCACTTAATGAATATAAAGAGCTGACGCG 1172
 DB 692 TTCACTTCCAGGCTGCTTAAACCACTTAATGAATATAAAGAGCTGACGCG 751

QY 1173 GGAAGCTGTGGAGCCAGACATCATCTGTGTAAAGAAAGAGAGATGTTGAGT 1232
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QY 1233 AATTTCACAAACCAATCCCTTGGAAACAGATACGATTCCTCAATCAAGGAGACGCA 1292
 DB 812 AATTTCACAAACCACTCCCTTGGAAACAGATACGATTCCTCAATCAAGGAGT 871

QY 1293 TTGGGGTTTTCTAGAGTGTG3-----AGATAAATGATGAGGAGCTGTAGCC 1343
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 DB 1529 AGGAGAGCATCTGCACAATATCTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCT 1588

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 DB 1589 GACTATATGCTCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1648

QY 2061 CACACAGAACTTCTCAAGCTGACGAGAGATGTCAAGTGAAGAAAGCTCAAGCTGT 2120
 DB 1649 TGTGAGAACTTCTCAAGCTGACGAGAGATGTCAAGTGAAGAAAGCTCAAGCTGT 1708

QY 2121 CAGATATGCTTCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2178
 DB 1709 CAGATATGCTTCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1768

QY 2179 TACTTCCCTTCCAGTACCAATGCTGTGTGACGACTTGA 2220
 DB 1769 TATCCCACTTACAGGAGAAACGCTGTGATGATCTCTGA 1810

RESULT 13
 ABA03201
 ID ABA03201 standard; cDNA; 2015 BP.
 XX
 AC ABA03201;
 DT 11-FEB-2002 (first entry)
 DE Human IL-17 receptor like protein #2 coding sequence.
 KW Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic;
 KW antipneumonia; antimicrobial; anorectic; neuroprotective;
 KW antiallergic; dermatological; cytostatic; gene therapy;
 KW interleukin 17; immune system disorder; infection; weight; reproductive;
 KW neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation;
 KW glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;
 KW tumour; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 50..1732
 FT /tag= a
 FT /product= "Human IL-17 receptor-like protein #2"
 PN WO200168705-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 16-MAR-2001; 2001MO-US08688.
 XX
 PR 16-MAR-2000; 2000US-189923P.
 PR 12-MAY-2000; 2000US-204208P.
 PR 27-NOV-2000; 2000US-0723232.
 PR 02-FEB-2001; 2001US-266159P.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Jing S, Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ;
 DR MPI: 2002-055100/07.
 DR F-PSDB; AAM47458.
 XX
 PT Three human nucleic acids encoding interleukin 17 (IL-17) receptor like
 PT polypeptides, useful for treating, diagnosing, ameliorating or
 PT preventing immune system disorders (e.g. psoriatic arthritis) and
 PT infections (e.g. viral infections)
 XX
 PS Claim 1; Fig 3; 23pp; English.
 XX
 CC The present invention relates to novel human nucleic acids encoding
 CC interleukin 17 (IL-17) receptor like proteins. The present sequence is
 CC one such coding sequence. The IL-17 receptor-like proteins and coding
 CC sequences are useful for treating a pathological condition related to
 CC immune system dysfunction (e.g. psoriatic arthritis), infections (e.g.
 CC viral infections), weight disorders (e.g. obesity), neuronal dysfunction
 CC disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin
 CC disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis),
 CC bone disease (e.g. osteoporosis), vascular system disorders (e.g.
 CC ischaemia), eye disorders, reproductive disorders, tumours and
 CC inflammation.
 CC
 SQ Sequence 2015 BP; 541 A; 499 C; 475 G; 500 T; 0 other;

Query Match 24.8%; Score 643.2; DB 24; Length 2015;
 Best Local Similarity 75.9%; Pred. No. 1.8e-18;
 Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;

QY 1233 AATTGACAAACCATCCCTTGAGAAAAGATACAGATTCTCATTCACGGGACACGACA 1292
DB 699 AACTTCACAACCACTCCCTGGGAAAAGATACATGCTCTTATCCACACAGCACTATC 758
QY 1293 TTGGGGTTTTCTAGATGCTGG-----AAGATTAATGATGAGAGCTGTAGCC 1343
DB 759 ATCGGGTTTTCTCAGGTTGTTGAGCCACACCAAGAAACAAACGAGCTTCAGTGTG 818
QY 1344 ATCCCGGTGACTGAGGAGTGAAGGTGCGGTGTTCAAGCTGACCCCATATTTACATACC 1403
DB 819 ATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGGTGACGTGACTCATATTTTCTACT 878
QY 1404 TGGGCAATGACTGCATCCGACGGAAGGACAGTTGTGCTTGTCTAGAGACAAGTCT 1463
DB 879 TGTGCGAGGAGCTGCATCCGACATTAAGGAAAGTTGTGCTGTGCCACAAACAGGCTC 938
QY 1464 CCCATCCCTCCAGATGACAAACAGACGATGCTGGAGGCTGGCTGCTCTTCCGTG 1523
DB 939 CTTTCCCTCTGATTAACAAACAAAGCAAGCCGGAGGCTGGCTGCTCTCTCTGCTG 998
QY 1524 ---CTGCTGGTGGCTGTGTGGGTGCTGCGAGCTGGGATCTAATTAACTTGAGGCAAGA 1580
DB 999 TCTCTGTGTGGTGGCCACATGGGTGTGTGTGGCAGGGATCTATTAATGTGAGGCAAGAA 1058
QY 1581 AGGAGCAGAAAGAGTCTTTCTTCTTATTTCCACAGTCTCTGCTCCCTCATTAAGTCTG 1640
DB 1059 AGGATCAAGAAAGACTTCTTTCTTA---CCACCACACTACTGCCCCCATTAAGTCTT 1115
QY 1641 GTCGTTTATCTCTGAGATATGTTTCCATCAACCGTCTGTGCTTCACTGACTTTCTT 1700
DB 1116 GTGGTTTACCCTGATTAATGTTTTCATCACACAAATTTTACTTCACTGAAATTTCTT 1175
QY 1701 CAAAATCTGCGAGAGTGAAGTCTCTTGAATAATGCGAAAAATGCGCGAG 1760
DB 1176 CAAAACCATTTGCGAAGTGAAGTCACTCTTGAATAATGCGAAAAATGCGAG 1235
QY 1761 ATGGGCGCGGTACAGTGGCTGACCACTCAGAAACGCGCAGATAAGTGTCTTCTT 1820
DB 1236 ATGGGTCCAGTGAAGTGGCTGCTGCACTCAAAAAGAGCAGACAAAGTGTCTTCTT 1295
QY 1821 CTTCCTCAGTGAAGTCCCGACCTTTGTGACAGTGTGCTGCGCAATGAGGCGAGCGCC 1880
DB 1296 CTTTCCAAATGACGTCAACAGTGTGCGATGTGCTGTGGCAAGCGAGGCGAGTCCC 1355
QY 1881 AGGAGAACTCTCAGGATCTGTCCTTCTTCTTAACTCTTTGTAGTATTCAGC 1940
DB 1356 AGTGAAGACTCTCAAGAA-CTTTCCCCCTTGCTTTTAACTTTTGTGAGTGAATTAAGA 1414
QY 1941 AGCCAGACGATCTGCAAAATACCTGTGTCTATCTTGGGGAGCAGACTCAAGGC 2000
DB 1415 AGCCAGATTCATCTGCAAAATACGTGTGTCTTACTTTAGAGAAATGATACAAAAGAC 1474
QY 2001 GACTATTAATGCTGTGAGTGTGCTGCCCCCAATATCATCTCATGAAGACGCAAGCTTTC 2060
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DB 1535 TGTGCAAACTTCTCATATGCAAGTGAAGGTGTGCAAGAAAGATCAAGGCTGC 1594
QY 2121 CATGATAGCTGTTCACCTGTGATGTCACCCGGGGGAA--TAGAGACTGTGAAGCTTCC 2178
DB 1595 CAGGATGGCTGTGCTGCTTGTGAGCCACCATGAGAGAGAAAGACCTTAAGGCTTCC 1654
QY 2179 TACTTCCCTTCCAGTGAACAAATGCTGTGTGAGACTTGAA 2220
DB 1655 TATCCCAACCAATTACAGGAAAAAAGTGTGATGATCTGAA 1696

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2003, 22:37:09 ; Search time 6593.47 Seconds
(without alignments)
11427.544 Million cell updates/sec

Title: US-09-778-971-4
Perfect score: 2589
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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3: gb_in:*
4: gb_om:*
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6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
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25: em_pl:*
26: em_ro:*
27: em_stg:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
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32: em_htg_other:*
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34: em_htg_pln:*
35: em_htg_rtd:*
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40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2589	100.0	2589	10	AF208109
2	1472.2	56.9	1963	10	AF208108
3	1449.6	56.0	2018	10	BC026546
4	991.6	38.3	234131	2	AC093357
5	644.8	24.9	1701	6	AX061651
6	644.8	24.9	1796	6	AX350967
7	644.8	24.9	1818	6	AX191534
8	644.8	24.9	2042	6	BC000980
9	643.2	24.8	1713	6	AX253209
10	643.2	24.8	1828	9	AF208110
11	643.2	24.8	1841	6	AX253204
12	643.2	24.8	1841	6	AX365258
13	643.2	24.8	2015	6	AX253207
14	643.2	24.8	2015	6	AX365260
15	634.4	24.5	1583	9	AF250309
16	632.2	24.4	637	6	AX350970
17	626	24.2	1816	9	AF212365
18	625.6	24.2	1509	6	AX191524
19	625.6	24.2	1515	6	AX092426
20	625.6	24.2	1515	6	AX180774
21	625.6	24.2	1515	6	AX376332
22	532.4	20.6	1506	6	AX350969
23	498.6	19.3	2856	9	AF208111
24	382	14.8	149634	9	AC113172
25	382	14.8	177072	9	AC012467
26	149.2	5.8	210	6	AX350972
27	147.6	5.7	374	6	AX098181
28	60	2.3	200885	2	AC012460
29	58	2.2	2584	9	AK095091
30	57.4	2.2	214694	2	AC130531
31	55.8	2.2	225633	2	AC105152
32	55.2	2.1	41339	9	AC005490
33	54.4	2.1	377	4	NME293350
34	54.4	2.1	182824	2	AC098153
35	54.2	2.1	185363	2	AC097617
36	54	2.1	164664	2	AC098211
37	54	2.1	187891	2	AC122021
38	53.6	2.1	200964	2	AL732553
39	53.6	2.1	230395	10	AL671878
40	53.4	2.1	156550	2	AC015830
41	53.4	2.1	166380	9	AC087237
42	53.2	2.1	207672	2	AC091263
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ALIGNMENTS

RESULT 1
AF208109 2589 bp mRNA linear ROD 17-JUL-2000
LOCUS AF208108 Mus musculus IL-17 receptor homolog short isoform precursor (Evi127)
DEFINITION mRNA, complete cds.

ACCESSION AF208109.1 GI:9246430
AF208109.1 GI:9246430

VERSION AF208109.1
KEYWORDS Mus musculus.
SOURCE Mus musculus.

ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2589)
Tian, E., Sawyer, J. R., Largaespada, D. A., Jenkins, N. A., Copeland, N. G.
and Staughtness, J. D. Jr.

Pred. No. is the number of results predicted by chance to have a

TITLE Evi17 encodes a novel membrane protein with homology to the IL17 receptor

JOURNAL Oncogene 19 (17), 2098-2109 (2000)

MEDLINE 20273223

PUBMED 10815801

REFERENCE 2 (bases 1 to 2589)

AUTHORS Shaughnessy, J.D. Jr.

TITLE Direct Submission

JOURNAL Submitted (24-NOV-1999) Myeloma and Transplantation Research Center, University of Arkansas for Medical Sciences, 4301 W. Markham St, Little Rock, AR 72212, USA

FEATURES

source Location/Qualifiers

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/db_xref="taxon:10090"

/chromosome="14"

1. .2589

/gene="Evi17"

/note="linked to ecotropic viral integration site 27"

19. .675

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/note="truncated; lacks transmembrane and cytoplasmic domains"

/codon_start=1

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/db_xref="GI:9246431"

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217. .219

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/note="putative; glycosylation site"

325. .327

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484. .486

/gene="Evi17"

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493. .495

/gene="Evi17"

/note="putative; glycosylation site"

501. .1132

/gene="Evi17"

/note="unspliced intron 7 in this isoform"

1317. .1321

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/note="putative"

2569

/gene="Evi17"

BASE COUNT 642 a 628 c 643 g 676 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GCCCTGCTGAGAGCGGACATATTCAGTGTGCTCTGAGACAGGCGCATCTCCAGAGTGG 120

QY 121 ATGTCCACACACACTCTCCAGAGACTTGAAGGAGCCTCCAACTGAACTGTCAG 180

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QY 181 ACAAGTGGCAGACAGAGAGGATTTTCATTTTGATTAACATTAAGCTGATCTCGGGCA 240

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QY 361 TCCGGCGCAATGACATTCCTCTATGAGGCTTCCGTGAGAGTGAAGTGAAGTGAAG 420

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DB 421 CTCATCAGCGCCCATTAACATCCCAATGCTAATGAATGAAGAGAGAGCCCTCTTGTCT 480

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DB 481 GTGAACCTTCACTCCGCGAGGTGCACTGCTGAACACAGAACTAACCTCCGCTATTT 540

QY 541 CCAGCAGCTAAACACAGAGCTCCGCGATTCAGCTCCCTTCCCAATTAATTCCTCT 600

DB 541 CCAGCAGCTAAACACAGAGCTCCGCGATTCAGCTCCCTTCCCAATTAATTCCTCT 600

QY 601 GGGCCAGAGACTCACTCACTCTGCGACCCAGCCTCTGCGCTGCTTTTCATGACTTT 660

DB 601 GGGCCAGAGACTCACTCACTCTGCGACCCAGCCTCTGCGCTGCTTTTCATGACTTT 660

QY 661 GTCAAACTTAAGTGTGTTCCATTCGAAATGTCGAAATGTCGAAATGTCGAAATGTC 720

DB 661 GTCAAACTTAAGTGTGTTCCATTCGAAATGTCGAAATGTCGAAATGTCGAAATGTC 720

QY 721 CCGGGATATGAGAGTGGGTATGAATCCACAGAGGAGCAGTAATCTTCTCATATGG 780

DB 721 CCGGGATATGAGAGTGGGTATGAATCCACAGAGGAGCAGTAATCTTCTCATATGG 780

QY 781 CCTATCTGGGCTGTGTGACATTTGTTGAGAGGCTGTGCTTATGAGCATCTGGTATCT 840

DB 781 CCTATCTGGGCTGTGTGACATTTGTTGAGAGGCTGTGCTTATGAGCATCTGGTATCT 840

QY 841 ACCACCTGAGCTTCACTGCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900

DB 841 ACCACCTGAGCTTCACTGCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900

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RESULT 2
 AF208108 1963 bp mRNA linear ROD 17-JUL-2000
 LOCUS
 DEFINITION Mus musculus IL-17 receptor homolog precursor (Evi27) mRNA,
 complete cds.
 ACCESSION AF208108
 VERSION AF208108.1 GI:9246428
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 SOURCE
 ORGANISM
 Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1963)
 Ian, E., Sawyer, J.R., Largespada, D.A., Jenkins, N.A., Copeland, N.G.
 and Shaughnessy, J.D. Jr.
 Evi27 encodes a novel membrane protein with homology to the IL17
 receptor

JOURNAL Oncogene 19 (17), 2098-2109 (2000)
 MEDLINE 20273223
 PUBMED 10815801
 REFERENCE 2 (bases 1 to 1963)
 AUTHORS Shaughnessy, J.D. Jr.
 TITLE Direct Submission
 JOURNAL Submitted (24-NOV-1999) Myeloma and Transplantation Research
 Center, University of Arkansas for Medical Sciences, 4301 W.
 Markham St, Little Rock, AR 72212, USA
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 location/Qualifiers
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 PDDRRLMGWLPFLVLVAWVLAAGIYLTMOGSTKTSPISTMLPLIKVLIV
 YPSRICHHNYRCPETDPLQNYCRSEVILEKKOKKIAEMGVPQMLTQOKADKVEL
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 3
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LOCUS         Mus musculus, interlentin 17b receptor, clone MGC:35924
DEFINITION    IMAGE:5042466, mRNA, complete cds.
ACCESSION     BC026546
VERSION       BC026546.1  GI:20071644
KEYWORDS      MGC.

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SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eulharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 2018)
TITLE	Strausberg, R.
JOURNAL	Direct Submission
COMMENT	Submitted (02-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
	Contact: MGC help desk
	Email: cgapdb-remail.nih.gov
	Tissue Procurement: Jeffrey E. Green, M.D.
	cDNA Library Preparation: Life Technologies, Inc.
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
	DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
	Web site: http://www-sbpc.stanford.edu
	Contact: (Dickson, Mark) mcdbpaxil.stanford.edu
	Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

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Qy      2553 CGTTGGAGACCTCTCAAAA 2573
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RESULT 4
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LOCUS      Mus musculus clone RP23-25A7, WORKING DRAFT SEQUENCE, 14 unordered
DEFINITION      pieces.
AC093357      1 GI:15213902
VERSION      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS      Mus musculus.
SOURCE      Mus musculus.
ORGANISM      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS      Birren, B., Linton, L., Nusbaum, C. and Lander, E.
JOURNAL      Unpublished
TITLE      2 (bases 1 to 234131)
REFERENCE      2 (bases 1 to 234131)
AUTHORS      Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
JOURNAL      Anderson, S., Barna, N., Bastien, V., Bonuslavsky, L., Bouhagalter, B.,
TITLE      Brown, A., Camarata, J., Campopiano, A., Chang, J., Chararo, B.,
AUTHORS      Choedel, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A.,
JOURNAL      Cooke, P., Dearlano, K., Dewar, K., Diaz, J., Dodge, S., Farr, S.,
TITLE      Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
AUTHORS      Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-pierre, N.,
JOURNAL      Hages, B., Heaford, A., Horton, L., Hulme, W., Ilev, I., Johnson, R.,
TITLE      Jones, C., Kamat, A., Karatas, A., Kellis, C., Laroque, K.,
AUTHORS      Lamasares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
JOURNAL      Maclean, C., Macdonald, P., Major, J., Marguis, N., Matthews, C.,
TITLE      McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J.,
AUTHORS      Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
JOURNAL      Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
TITLE      Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
AUTHORS      Raymond, C., Retta, R., Riback, M., Riley, R., Rise, C., Rogov, P.,
JOURNAL      Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R.,
TITLE      Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
AUTHORS      Strauss, N., Subramanian, A., Talamas, J., Testafaye, S., Theodore, J.,
JOURNAL      Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,
TITLE      Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G.,
AUTHORS      Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
JOURNAL      Direct Submission
TITLE      Submitted (20-AUG-2001) Whitehead Institute/MIT Center for Genome
JOURNAL      Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT      All repeats were identified using RepeatMasker:
COMMENT      http://ftp.genome.washington.edu/RM/RepeatMasker.html

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TITLE      Center: Whitehead Institute/ MIT Center for Genome Research
JOURNAL      Center code: MIBR
COMMENT      Web site: http://www-seq.wi.mit.edu
JOURNAL      Contact: sequence_submissions@genome.wi.mit.edu
JOURNAL      Project Information
JOURNAL      Center project name: l13729
JOURNAL      Center clone name: 25 A 7
JOURNAL      Summary Statistics
JOURNAL      Sequencing vector: Plasmid; n/a; 100% of reads
JOURNAL      Chemistry: Dye-terminator Big Dye; 100% of reads
JOURNAL      Assembly program: Phrap; version 0.960731

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FEATURES

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             Consensus quality: 231921 bases at least Q20
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             Insert size: 232831; sum-of-contigs
             Quality coverage: 10.4 in Q20 bases; agarose-fp
             Quality coverage: 9.4 in Q20 bases; sum-of-contigs
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             * NOTE: This is a 'working draft' sequence. It currently
             * consists of 14 contigs. The true order of the pieces
             * is not known and their order in this sequence record is
             * arbitrary. Gaps between the contigs are represented as
             * runs of N, but the exact sizes of the gaps are unknown.
             * This record will be updated with the finished sequence
             * as soon as it is available and the accession number will
             * be preserved.
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LOCUS DEPOSITION
ACCESSION AX350967 Sequence 1 from Patent WO0190358.
VERSION AX350967.1 GI:18616343
KEYWORDS
ORGANISM unidentified.
SOURCE unidentified.
REFERENCE 1
AUTHORS Gorman, D.M.
TITLE Mammalian receptor proteins; related reagents and methods
JOURNAL Patent: WO 0190358-A 1 29-NOV-2001;
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DEFINITION Sequence 56 from Patent WO0149728.
ACCESSION AX191534
VERSION AX191534.1 GI:15209721
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1818)
AUTHORS Kato,S., and Kimura,T.
TITLE Human proteins having hydrophobic domains and dnas encoding these
JOURNAL Protein
Patent: WO 0149728-A 56 12-JUL-2001;
Location: SAGAMI CHEMICAL RESEARCH CENTER (JP)
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Query Match 24.9%; Score 644.8; DB 6; Length 1818;
Best Local Similarity 76.0%; Pred. No. 4e-192;
Matches 853; Conservative 0; Mismatches 252; Indels 17; Gaps 4;
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ACCESSION BC000980
VERSION BC000980.1 GI:12654318
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 2042)
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
REMARK
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalob@bcm.tmc.edu
Villalob, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Hollway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAX Plate: 3 Row: n Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9246432.
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BASE COUNT 625 a 484 c 426 g 507 t

Query Match 24.9%; Score 644.8; DB 9; Length 2042;
Best Local Similarity 76.0%; Pred. No. 4,1e-192;
Matches 853; Conservative 0; Mismatches 252; Indels 17; Gaps 4;

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QY 2179 TACTCTCTTCACTGACAAATGCTGTGTGACACTGTGA 2220

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RESULT 9
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LOCUS AX253209 1713 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 6 from Patent WO0168705.
ACCESSION AX253209
VERSION AX253209.1 GI:15986350
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1713)
Jing,S., Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S. and
Nguyen,H.O.
11-17 receptor like molecules and uses thereof
Patent: WO 0168705-A 6 20-SEP-2001;
JOURNAL Amgen Inc. (US)
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Query Match 24.8%; Score 643.2; DB 6; Length 1713;
Best Local Similarity 75.9%; Pred. No. 1.3e-191;
Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;
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 complete cds.
 ACCESSION AF208110
 VERSION AF208110.1 GI:9246432
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 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 1828)
 Tian,E., Sawyer,J.R., Largaespada,D.A., Jenkins,N.A., Copeland,N.G.
 and Shaughnessy,J.D., Jr.
 EVI27 encodes a novel membrane protein with homology to the IL17
 receptor
 JOURNAL Oncogene 19 (17), 2098-2109 (2000)
 MEDLINE 20273223
 PUBMED 10815801
 REFERENCE
 2 (bases 1 to 1828)
 Shaughnessy,J.D. Jr.
 TITLE Direct Submission
 JOURNAL Submitted (24-NOV-1999) Myeloma and Transplantation Research
 Center, University of Arkansas for Medical Sciences, 4301 W.
 Markham St, Little Rock, AR 72221, USA
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Best Local Similarity 75.9%; Pred. No. 1.3e-191;
Matches 852; Conservative 0; Mismatches 253; Indels 17; Gaps 4;
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LOCUS
DEFINITION Sequence 1 from Patent WO0168705.
ACCESSION AX253204
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VERSION      AX253204.1  GI:15986346
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SOURCE       human.
ORGANISM     Homo sapiens
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AUTHORS     1 (bases 1 to 1611)
              Jing,S., Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S. and
              Nguyen,H.Q.
              11-17 receptor like molecules and uses thereof
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BASE COUNT   522 a 455 c 416 g 448 t
ORIGIN
Query Match      24.8%  Score 643.2;  DB 6;  Length 1841;
Best Local Similarity 75.9%;  Pred. No. 1.3e-191;
Matches 852;  Conservative 0;  Mismatches 253;  Indels 17;  Gaps 4;

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VERSION      AX365258.1  GI:18697003
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              Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S., Nguyen,H.Q. and
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 REFERENCE 1 (bases 1 to 1583)
 AUTHORS Zhang, W. and Cao, X.
 TITLE Direct Submission
 JOURNAL Submitted (29-MAR-2000) Department of Immunology, Second Military Medical University, and Shanghai Brilliance Biotechnology Institute, 800 Xiangyin Rd., Shanghai 200433, P.R. China
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